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Molecular cloning of mesothelin, a
mesotheliomas, and
                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (09-NOV-1995) Kai Chang, Laboratory of Molecular Submitted (19-NOV-1995) Kai Chang, Laboratory of Molecular National Cancer Institute, Building 37, Room 4B19, 37 Convenience, MSC4255, Bethesda, MD MD20892-4255, USA
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LPAALACWGYWGSLLSEADVRALGGLACDLPGRFVARESAEVLLDERLYSCPGPLDQDQ
EARRAALQGGGPPYGPPSTWSVSTMADALRGLLPVLGQPIIRSIPPGGTVAAWRGRSSRD
BARRAALQGGGPYGPPSTWSVSTMADALRGLLPVLGQPIIRSIPPGGTVAAMICRESRD
PSWRQPERTILRPRFFRREVEKTACPSGKKAREIDESLIFYKKWELEACVDAALLATQM
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                                                                PLGGVLTTPHNISSLSPRQLLGFPCAEVSGLSTERVRELAVALAQKNVKLSTEQLRCL
                                                                                                                                                                                              /cell_type="HeLa"
/tissue +v>^-"
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/chromosome="16"
                                                                                                /protein_id="AAC50348
/db_xref="GI:1145724"
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SPEELSSVPPSSIMAVRPQDLDTCDPRQLDVLFVKARLAFQNNMGSEYPKVLQSFLGG
APTEDLKALSQQNVSHDLATFMKLRTDAVLPLTVAEVQKLLGBHVEGLKAEERHRPVR
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GENE CODING MAGAKARYOCYTE AMPLIFIER
L Patent: JP 1994225767-A 1 15-AUG-1994;
CHUGAI PHARMACEUT CO LTD
OS Homo sapiens (human)
PN JP 1994225767-A/1
PD 16-AUG-1994
PF 25-OCT-1993 JP 1993288617
PR 23-OCT-1993 JP 1993288617
PR 23-OCT-1992 JP 92P 286153, 11-NOV-1992 JP 92P
09-DEC-1993 JP 1993288617
PR 23-OCT-1993 JP 1993288617
PR 23-OCT-1993 JP 1993288617
PR 23-OCT-1993 JP 1993288617
PR 23-OCT-1993 JP 92P 286153, 11-NOV-1992 JP 92F
09-DEC-1993 JP 93P 329546
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PC C12N15/16,C12N1/21,C12N5/10,C12P21/02//A61K37/02,C07K13/00, PC C1201/68,
PC (C12N1/21,C12R1:19),(C12N5/10,C12R1:91),(C12P21/02,C12R1:19),
PC (C12N1/21,C12R1:19),(C12N5/10,C12R1:91),(C12P21/02,C12R1:19),
PC (C12R1:91),
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THE THE TOCOCO PPC
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1 (bases 1 to 2129)
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Homo sapiens
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JP 1994225767-A/1.
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/cell_line='HPC-Y5'
/clone='pKPO27'
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/db_xref="taxon:9606"
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3GG 1798 3GG 1777	QY 1739 AACITCIGGACCCCACGIGGAGGCCTGAAGGCGGAGGAGCGGCACCGCCCGGIGCG
AGA 1738 AGA 1717	Qy 1679 CCACGTTCATGAAGCTGCGGACGGATGCGGTGCTGCCGTTGACTGTGGCTGAGGTGCA
rgg 1678 rgg 1657	Oy 1619 GTGGGGCCCCCACGGAGGATTTGAAGGCCCTCAGTCAGCAGAATGTGAGCATGGACTT Db 1598 GTGGGGCCCCCACGGAGGATTTGAAGGCCCTCAGTCAGCAGAATGTGAGCATGGACTT
rgg 1618 rgg 1597	155 153
CCC 1558	Qy 1499. GGCCCCAGGACCTGGACACGTGTGACCCAAGGCAGCTGGACGTCCTCTATCCCAAGGC
TCA 1498 CA 1477	439
ACC 1438 ACC 1417	1379 GAAGGGCCAGCTAGACAAAGACACCCTAGACACCCTGACCGCCTTCTACCCTGGGT
AGG 1378 AGG 1357	319 CTCAGGCTCCTCGGCGGCC
STC 1318 STC 1321	1259 TGACGTCCCTGGAGACCCTGAAGGCTTTGCTTG
ATG 1258 ATG 1261	Qy 1199 TCCAGCACCTGGGCTACCTCTTCCTCAAGATGAGCCCTGAGGACATTCGCAAGTGGAA
TGA 1198 TGA 1201	139 TGGACGTCCTAAAGCATAAACTGGATGAGCTCTACCCACAAGGTTACCCCGAGTCTG
AGC 1138 AGC 1141	1079. CGGCCCTGCTGGCCACCCAGATGGACCGCGTGAACGCCATCCCCTTCACCTACGAGC
ATG 1078 ATG 1081	1019 GCGAGATAGACGAGAGCCTCATCTTCTACAAGAAGTGGGAGCTGGAAGCCTGCGTGG
CCC 1018 CCC 1021	Qy. 959 TCCGGCCGCGGTTCCGGCGGGAAGTGGAGAAGACAGCCTGTCCTTCAGGCAAGAAGGG
TCC 958	99 CCGCGTGGCGGCAACGCTCCTCTCGGGACCCATCCTGGCGGCAGCCTGAACGGACCA .
rgg 898 rgg 901	839 GGGCCTGCTGCCCGTGCTGGGCCAGCCCATCATCCGCAGCATCCCCAGGGCATCG
TGC 841	782 GCGGGGGACCCCCTACGGCCCCCGTCGACATGGTCTGTCT

Db 2 AATTCGGCACGAGGCCACTCCCGTCTGACCGCGGCACAGAGAGCTACCGGTGGAC 61 Oy 65 CCACGGTGCCTCCCTCCCTGGGATCTACACAGACCATGGCCTTG-CAACGGCTCGACCCC 123	SE COUNTIGIN IGIN Query Ma Best Loc Matches	RESULT 5 189985 189985 189985 189985 ACCESSION Sequence 34 from patent US 5723318. ACCESSION 189985 VERSION 189985,1 GI:3409925 KEYWORDS SOURCE Unknown. ORGANISM Unknown. REFERENCE 1 (bases 1 to 2129) AUTHORS Yamaguchi, N., Kojima, T., Oh-eda, M. and Hattori, K. TITLE DNA coding for megakaryocyte potentiator JOURNAL Patent: US 5723318-A 34 03-MAR-1998; FEATURES Location/Qualifiers SOURCE 1.2129	1919 1898 1979 1958 2039 2018 2018
1139 TGGACGTCCTAAAGCATAAACTGGATGACCTCTACCCACAAGGTTACCCCAGAGTTGTGAAAACTGGATGACCTCTACCCACAAGGTTACCCCAGAGTTACCCCAGAGTTGTGAAAACTGGATGAACTTGAACTTGAACTTGACCACAAAGGTTACCCCAGAGTTACCCCAGAGTTGACCAGAGTTACCCCGAGTTCGTGAAAACTGAAACTTGAATGAA	Qy 959 TCCGGCCGCGGTTCCGGCGGGAAGTGGAGAAGACAGCCTCTCAGGCAAGAAGACAGCCC 1018	Oy 719 TGAGCTGCCCGGACCCCTGGACCAGGACCAGCAGCCAGGCCGCCTCTGCAGG 778 11111111111111111111111111111111111	422 CTGAGCCCCCCAGGACCTGGACGCCTCCCATTGGACCTGCTATTCCTCAACCCAG 479 ATGCGTTCTCGGGGCCCCAGGCCTGCACCCGTTTCTTCTCCCGCATCACGAAGGCCAATG [

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Gene Collection (MGC), Cance
Institute, 31 Center Drive,
Steven Jones, Jennifer Asano, Ian Susanna Chan, Readman Chiu, Chris Letticia Hsiao, Martin Krzywinski,
                                                                  cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Co DNA Sequencing by: Genome Sequence Centre,
                                                                                                        NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
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BC003512
                                       BC Cancer Agency, Vancouver, info@bcgsc.bc.ca
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366 GAAGAATGTCAAGCTCTCAACAGAGCAGCTGCGCTGTCTGGCTCACCGGCTCTCTGAGCC

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ALSOONVSMDLATEMKLHTDAVALPLTVAEVQKLLGPHVEGLKAEERHRPVRDWILKOR
QDDLDTLGLGLGGGIPKSYLVLDLSVYQEALSGTPCLLGPGPVLTVLALLLASTLA"
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DPSWRQPERTILRPRFRREVEKTACPSGKKAREIDESLIFYKKWELEACVDAALLATQ
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Lipaalacwgvrgsllseadvralgglacollpgrfvaesaevllprlvscpgpldodo
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/db_xref="GI:13097582"
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J. Biol. Che
95394969
2 (bases 1
Kojima, T.
Kojima, T.
Direct Submission
Submitted (23-FEB-1995) to the
Kojima, Chugai Pharmaceutical
Laboratories; 1-135 Komakado,
                                                                                                                                                                                                    Homo sapiens pancreatic cancer cell cell_line:HPC-Y5 clone:pKPO27.
                                                    Unpublished
3 (bases 1
                                                                                                                             and Yamaguchi, N.
Molecular cloning and
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Mammalla; Eutheria; Primates;
1 (bases 11 to 2093)
Kojima,T., Oh-eda,M., Hattori
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D49441 GI:1129078
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Location/Qualifiers
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/db_xref="taxon:9606"
/cell_line="HPC-Y5"
/cell_type="pancreatic ca:
/clone="pkPO27"
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QQEAARAALQGGGPPYGPPSTWSVSTWDALRGLLPVLGOPIIRSIPGGIVAAWRQRSS
RDPSWRQPERTILRPREREVEKTACPSGKKAREIDESLIFYKKWELLACVDAALLAT
QMDRVNAIPFTYEQLLDVLKHKLDELYPOGYPESVIQHLGYLFILKMSPEDIRKWNVTSL
ETLKALLEVNKGHEMSPOVATLIDREVKGRGQLDKDTLDTLTAFYPGYLCSLSPEELS
SYPPSSIWAVRPQDLDTCDPRQLDVLYRKARLAFQNMNGSEYFVKIQSFLGGAPTEDL
KALSQONVSMDLATFMKLRTDAVLPLTVAEVQKLLGPHVEGLKAEERHRPVRDMILRQ
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192. 950
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BC009272
BC009272.1
web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov
Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,
Dietrich,N.L., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspl,R.,
Lim,M., Maduro,Q.L., Masiello,C., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J.,
                                                                                                  DNA Sequencing by: National Sequencing Center (NISC), Gaithersburg, Maryland;
                                                                                                                             cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramur
                                                                                                                                                                                                    USA
NIH-MGC Project URL: http://mgc.
Contact: MGC help desk
                                                                                                                                                                                                                                              Direct Submission
Submitted (12-JUN-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae,
                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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Clone distribution: MGC clone distribution information through the I.M.A.G.E. Consortium/LLL at: http://imag Series: IRAL Plate: 15 Row: j Collumn: 2
This clone was selected for full length sequencing becaused the following selection criteria: matched mRNA
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                                           416
/product="Unknown (protein for MGC:10273)"
/protein_id="AAH09272.1"
/db_xref="GI:1424505"
/db_xref="GI:1424505"
/db_xref="GI:14424505"
/db_xref="GI:1424505"
/dr_xref="GI:142450
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/db_xref="taxon:9606"
/clone="MGC:10273 IMAGE:3957372"
/tissue_type="Placenta, choriocarc
/clone_lb="NJH_MGC_21"
/lab_host="DH10B-R"
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Local Sinhes 2039; CGGGAGCTGTGGCCTTGGCACAGAAGAATGTCAAGCTCTCAACAGAGCAGCTGCGC CTGCTATTCCTCAACCCAGATGCGTTCTCGGGGCCCCAGGCCTGCACCCGTTTCTTCTCC CTGCTATTCCTCAACCCAGATGCGTTCTCCGGGGCCCCAGGCCTGCACCCGTTTCTTCTCC CGGGAGCTGGCCTTGGCCACAGAAGAATGTCAAGCTCTCAACAGAGCAGCTGCGC CCTCGCCAACTCCTTGGCTTCCCGTGTGCGGAGGTGTCCGGCCTGAGCACGGAGCGTGTC CCTCGCCAACTCCTTGGCTTCCCGTGTGCGGAGGTGTCCGGCCTGAGCACGGAGCGTGTC CAGGAGGCTGCGCCCTGGACGGAGTCCTGGCCAACCCACCTAACATTTCCAGCCTCTCC ACGGAGTCTGCCCCCCTGGGGGGGAGTCCTGACAACCCCCCATAACATTTCCAGCCTCTCC CAGAGAGCTACCGGTGGACCCACGGTGCCTCCCTCCCTGGGATCTACACAGACCATGGCC Similarity Conservative 91.7**%**; 97.1**%**; 0; Score Pred. Mismatches NO. 1961; No. 0; DB 9. 30; Length 2162; Indels 30; Gaps 459 122 542 519 482 182 159 399 362 339 302 279 242 219

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                     GTCCTCTATCCCAAGGCCCGCCTTGCTTTCCAGAACATGAACGGGTCCGAATACTTCGTG
                                                                 ATCGACCGCTTTGTGAAGGGAAGGGGCCAGCTAGACAAAGACACCCTAGACACCCTGACC
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Direct Submission
Submitted (26-AUG-1999) T
511, Seattle, WA 98107, U
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 1195)
Scholler, N., Fu, N., Yang, Y., Ye, Z., Goodman, G.E., He
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Soluble member(s)
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/db_xref="taxon:9606"
/translation="vektacpsgkkareideslifykkweleacvdaallatomdrvn
aipftyeqldvlkhkldelypogypesviohlgylflkmspedirkwnvtsletlkal
                                           /codon_start=1
/product="mesothelin/megakaryocyte
/protein_id="AAF01409.1"
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NVSMDLATEMKLRTDAVLPLTVAEVOKLLGPHVEGLKAEERHRPVRDWILRORODDLD
TLGIGLQGGIPNGYLVLDLSVQGGRGGQARAGGRAGGYEVGALSHPSLCRGPLGDALP
PRIWTCSHRPGTAPSLHPGLRAPLPCWPQPCWGSPPGQEQARVIPVPPQENSRSVNGN
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Pred. No. 3.1
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3.8e-164;
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CLARRLPRHLTDEELNALPLDLLLFLNPAMFPGQQACAHFFSLISKANVDVLPRRSLE

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	FEAT	ME JO	TI	AU	JO	REFE AU		JO	11.0	REFE	OR.	KEYW	ACCE	LOCUS	RESU D863	Б	Qy	Db	Qy	рь	Qy	DЬ	Qy	Ф	Qy	рь	Qy
sig_pep CDS	EATURES Source	JOURNAL MEDLINE	ITLE	THORS	TITLE JOURNAL	EFERENCE AUTHORS		URNAL	TITLE	RENCE	ORGANISM	KEYWORDS SOURCE	SSION	S S	ULT 10	1177	2100	1117	2040	1057	1980	997	1920	937	1899	877	1882
eptide 109. 1255 109. 1986 109. 1986 /function="stimulates the megakasryocyte colony forming activity of murine interleukin-3 in mouse bone marrow cell culture" /codon_start=1 /product="megakaryocyte potentiating factor" /protein_id="BAA13077.1" /db_xref="01:1408517" /translation="MALPTARRELIGSCGSPICSRSFLLLLISLGWIPRLQTQTTKTSQEATLLHAVNGAADFASLFTGLFIGLTCEEYSDLSMEQAKGLAMAVRQKNITLRGHQLR		J. Biol. Chem. 270 (37), 21984-21990 (1995) 95394969	Molecular cloning and expression of megakaryocyte potentiating factor cDNA	o (Silves) Kojima, T., Oh-eda, M., Hattori, K., Taniguchi, Y., Tamura, M., Ochi, N. and Yamaguchi, N	mouse Megakaryocyte Potentiating Factor cDNA Unpublished (1996)	2 (bases 1 to 2135) Kojima,T., Taniguchi,Y., Hattori,K. and Oh-eda,M.	Cytokine Research Program; 153-2, Nagai, Niihari, Ibaraki 300-41, Japan (E-mail:kojimat@mb.infoweb.or.jp, Tel:0298-30-6211, Fax:0298-30-6270)	nBank databases. Tet ular Medicine, Inc.,		Muridae; Murinae; Mu	<pre>Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;</pre>		D86370 1 GT-1408516	D86370 2135 bp mRNA ROD mouse mRNA for megakaryogyte potentiating factor		ATGCCCCCTGCAGACA 1192	ATGCCCCCTGCAGACA 2115	GAGCAGGCACGGGTGATCCCCGTTCCACCCCAAGAGAACTCGCGGCTCAGTAAACGGGAAC 1176	GAGCAGGCACGGGTGATCCCCGTTCCACCCCAAGAGAACTCGCGCTCAGTAAACGGGAAC 2099	GCCTGAGGGCCCCACTCCCTTGCTGGCCCCAGCCCTGCTGGGGATCCCCGCCTGGCCAG 1116		CTGCCTCCTAGGACCTGGACCTGTTCTCACCGTCCTGGCACTGCTCCTAGCCTCCACCCT 1056	CTGCCTCCTAGGACCTGGACCTGTTCTCAGCGTCCTGGCACTGCTCCTAGCCTCCACCCT 1979	GCCGTGGAGGTGGGCCCTCTGAGTCACCCCCTCTCTCTGTAGAGGCCCTCTCGGGGACGCC 996	AGAGACCCTCTCGGGGACGCC 1919	TITITITITITI	CTAGACCTCAGCGTGCA 1898

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                                                                                                          GAGGAGTGGAAGAACCCAATATGGCCCCCCATCGAAGTGGTCAGTCTCCACCCTGGATGC
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OSQEKAVNEVLRSGRTQYGPPSKWSVSTLDALQSLVAVIDESIYDGSIEKDVKAEWLQH
ISRDPSRLGSKLTVIHPRFRRDADGKACPPGKERPYKDEDLIFYQNWELEACVDGTWL
ARQMDLVNEIPFTYEQLSIFKHKLDKTYPQGYEESLIQQLGHFFRYVSPEDIHQWNVT
SPDTVKTLKVSKGQKWAQALALVACYLRGGGOLDEDWYKALGDIPLSYLCDFSPQD
LHSVPSSVMWLVGPODLDKCSORHLGLLYQKACSAFQNVSGLEYFEKIKTFLGGASVK
DLRALSQHNVSMDIATFKRLQVDSLVGLSVAEVQKLLGPNIVDLKTEEDKSPVEDWLF
S**QHQKDLDRLGGGIPNGYLVLDFNVREAPSSRASLLGPGFVLIWIPALLPALRL
S**QHQKDLDRLGLGLQGGIPNGYLVLDFNVREAPSSRASLLGPGFVLIWIPALLPALRL
S**QHQKDLDRLGLGLQGGIPNGYLVLDFNVREAPSSRASLLGPGFVLIWIPALLPALRL
S**QHQKDLDRLGLGLQGGIPNGYLVLDFNVREAPSSRASLLGPGFVLIWIPALLPALRL
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S**QHQKDLDRLGLGLGLGGIPNGYLVLDFNVREAPSSRASLLGPGFVLIWIPALLPALRL
S**QHQKDLDRLGLGLGLGGIPNGYLVLDFNVREAPSSRASLLGPGFVLIWIPALLPALRL
S**QHQKDLDRLGLGLGGIPNGYLVLDFNVREAPSSRASLLGPGFVLIWIPALLPALRL
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1970	GACGCCCTGCCTAGGACCTGGACCTGTCTCACCGTCCTGGCACTGCTCCTAGC	1914	Qy
1970		1911	Db
1913	GGGCGGCATCCCCAACGGCTACCTGGTCCTAGACCTCAGCGTGCAAGAGACCCTCTCGGG	1854	Qу
1910		1851	ФЪ
1853 1850	GCGGGACTGGATCCTACGGCAGCGGCAGGACGACGACCTGGGGCTGGGGCTGCGGCTGCACACACA	1794 1791	ОУ
179 179	GCGGAGGAGCGCACCGCCC ACCGAGGAGGATAAAAGCCC	1734 1731	Фр
173	CETTCATGAAGCTGCGGACGGACGGCGGTGCCGTTGACTGTGGCTG	1674	. Qу
173		1671	Db
7	CTGGGTGGGGCCCCCACGGAGGATTTGAAGGCGCTCAGTCAG	0 0	Qy Db
	CGCCTTGCTTTCCAGAACATGKACGUGTCCGAATACTTCGTGAAGATCCAGTC	ທ ທ	Оу
55	GGTCAGGCCCCAGGACCTGGACACGTGTGACCCAAGGCAGCTGGACGTCCTCTATCCCAA	4 4	Оу
1493	GTACCTGTGCTCCCTCAGCCCCGAGGAGCTGAGCTCCGTGCCCCCCAGCAGCATCTGGGC	1434	Qy
1490		1431	Db
	CTAGACAAAGACACCCTAGACACCCTGACCGCTTCTACCCT	1374	Qy
		1371	Db
1373 1370	GAGTCCTCAGGCTCCTCGGCGGCCCCTCCCACAGGTGGCCACCCTGATCGACCGCTTTGT	1314 1335	Оу
1313	GAATGTGACGTCCCTGGAGACCCTGAAGCTTTGCTTGAAGTCGACAAAGGGCACGAAAT	1254	Qy
1334		1275	Db
1253	TGTGATCCAGCACCTGGGCTACCTCTTCCTCAAGATGAGCCCTGAGGACATTCGCAAGTG	1194	Qy
1274		1215	Db
1193 1214	GCAGCTGGACGTCCTAAAGCATAAACTGGATGAGCTCTACCCACAAGGTTACCCCGAGTC	1134 1155	Qy Db
1133	GGATGCGGCCCTGCTGGCCACCCAGATGGACCGCGTGAACGCCATCCCCTTCACCTACGA	1074	Qу
1154		1095	рь
1073	GGCCCGCGAGATAGACGAGAGCCTCATCTTCTACAAGAAGTGGGAGCTGGAAGCCTGCGT	1014	Qy
1094		1035	Db
1013 1034	CATCCTCCGGCCGCGGTTCCGGCGGGAAGTGGAGAAGACAGCCTGTCCTTCAGGCAAGAA 1 1 1 1 1 1 1 1 1	954 975	Фр
953	CGTGGCCGCGTGGCGGCAACGCTCCTCGGGACCCATCCTGGCGGCAGCCTGAACGGAC	894	Qy
974		915	Db

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (23-AUG-1996) to the DDBJ/EMBL/GenBank databases. Hino, Cancer Institute, Department of Experimental Patholog Kami-Ikebukuro 1-37-1, Toshima-ku, Tokyo 170-8455, Japan (E-mail:ohino@ims.u-tokyo.ac.jp, Tel:03-5394-3815,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yamashita, Y., Yokoyama, M., Kobayashi, E., Takai, S. and Hi
Mapping and determination of the cDNA sequence of the Er
preferentially expressed in renal cell carcinoma in the
mutant (Eker) rat model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biochem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                 CLARRLPKHLTNEELDALPLDILLF-LIVPAMFGGQQACAHF-SSLITSKAAWNUFURSILE
RORLLTGALKCOGVYGFOVSETDARALGGLACDLPGEFVAKSSEVLLPWLARCGGPLD
GQQAKAVREVLKSGRAPYGPPSTWSVSTLDALQGLLVVLDESTVHSIPKDVTITEWLQG
ISREPSRLGSKWTVTHPFFRRDTEQKACPPGKEPNVVDRILIFYQNWELBACVDGTLL
AGQMDLVNEIFTYEQLSIFKIKLDKYYPQGYPESLIKQLGHFFRYVSPEDIKQWNVT
SPDTVNTLLKVSKGQKMDAQVIALVACYLRGGGKLDEDIVKALDNIPLSYLCDFSPQD
LHAIFSSVMWLVGLHDLDKCSQRHLGILYQKACSAFQNVSGLEYFEKIRTFLGGASRE
DLRALSQHNVSMDIATFKKLQVDALVGLSVAASVAFQRVTGGHTGDLKTEEDKSPVRDWLF
RQQQKDLDSLGLGLQGGIPNGYLILDFNVREAFSSGAPLLGPGFVFAMIPALLSALRL
ST
                                                                                                                                                                                                                                                                                                                                                                           /gene="Erc"
91. .1968
                                                                                                                                                                                                                /translation="MALPTAQPLLGSCGSPICSRSFLLLLLSLGWLPLLQTQTTRTSQ
EAALLHAVTGTVDFASLPTGLFLGLTCDEVSGLSMGHAKELAMAVRQKNIVLQVHQLR
                                                                                                                                                                                                                                                 /product="mesothelin"
/protein_id="BAB13512.1"
/db_xref="GI:10129878"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:10116"
/cell_line="ERC33"
                                                                                                                                                                                                                                                                                                                       (MPF)"
                                                                                                                                                                                                                                                                                                                                        /note="homologue
                                                                                                                                                                                                                                                                                                                                                        /gene="
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /strain="Eker rat"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                      /codon_start=1
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                                                                                                          TTTAAGACTGAGCTGAGACCACCACCTCCTAAGGCTCCTGGTCCCAGCTCTATTGTCGAGC
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/note="Alusx repeat: F
1991..2128
/note="FLAM_C repeat:
2332..2626
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                                                              1620. .193:
                                                                                                                                                       /note="THE1C repeat:
200. .510
                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                          /note="AluJb
                                                                                            741. .1033
                                                                                                         /note="THE1C repeat:
                                                                                                                                    /note="AluSq repeat:
                                                                                                                                                                                                  /clone="LA16-335H7"
/clone_lib="LA16"
                                                                                                                                                                                                                                  /chromosome="16"
                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
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requests: clonerequest@sanger.ac.uk

On Apr 22, 2001 this sequence version replaced gi:9798432.

During sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats: all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em. EMBL; Sw.;
SMISSPROT; Tr., TREMBL; Wp., WORMPEP; Information on the WORMPEP
database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://www.sanger.ac.uk/Projects/C_elegans/wormpep LA16-35H7 is part of a clone contig from the tip of the short arm of chromosome 16 spanning 2Mb of pl3.3 (Higgs D.R., Flint J., Daniels R., MRC Molecular Haematology Unit, Institute of Molecular Medicine, Oxford (unpublished)), and is from the Los Alamos, flow sorted human Chromosome 16 libraries constructed by Norman Dogett (unpublished). VECTOR: SCOS-1 (unpublished). VECTOR: SCOS-1 IMPORTANT: This sequence is not the entire insert of clone LA16-335H7 it may be shorter because we sequence overlapping sections only once, except for a 100 base overlap.

The true left end of clone LA16-32ID2 is at 37208 in this sequence. The true right end of clone LA16-32ID2 is at 5146 in this sequence. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (17-APR-2001) Sanger Centre, Hinxton,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UK. E-mail enquiries: humquery@sanger.ac.uk
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/note="L1"
7004
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2638. .2929
/note="AluSg repeat: matches 5.
                                                                                                                   /note="Aluyb8 repeat: matches 10. .132 of consensus"
11500. .11803
                                                                                                                                                    /note="Alux repeat: matches 1. .295 of consensus" 11372. .11499
                                                                                                                                                                                   /note="L1ME2 repeat: matches 4946.
11048. .11336
                                                                                                                                                                                                                                                                                                                                                                                      9679. .9969
/note="AluJo repeat: matches 2.
9970. .10029
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/note="MER49 repeat: matches 5. .285 of consensus"
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/note="AluY repeat: matches 1.
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/note="AluSq repeat:
/note="match: GSS: Em:AQ166427"
                                                                                note="Alux repeat:
11805. .12112
                                                                                                                                                                                                                                  10747. .10844

note="Lime2 repeat: matches 5162.
                                                                                                                                                                                                                                                         10230. 10530
/note="Alusx repeat: matches 1. .302 of consensus"
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/note="L1MB8 repeat: matches 6126.
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'note="AluSx repeat: matches l. .294 of consensus"
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/note="L1MB4 repeat: matches 5518.
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/note="MER4D repeat:
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/note="L1MB4 repeat:
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note="AluSx repeat:
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/note="AluSx repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                       note="L1M4 repeat:
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note="L1ME2 repeat: matches 5402.
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                                                                  'note="AluSx repeat: matches 1.
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note="L1MA10 repeat: matches 6252. 6322 of consensus"
                                                                                                                                                                                                                                                                                                                                                                   note="L1M4 repeat: matches 5314. .5379 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7. .8894
te="L1MA10 repeat: matches 6172. .6252 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8. .8433
te-"AluSq/x repeat: matches 1. .136 of consensus"
                                                                                                                                                                                                                                                                                                      te="AluSq/x repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          .9678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .1M4 repeat: matches 5490.
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                                 repeat:
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                                                                                                                                                                                                                                                                               Query Match 14.4%;
Best Local Similarity 82.4%;
                                                                                                                                                       21310
                                                                                                                                                                            1710 GCTGCCGTTGACTGTGGCTGAGGTGCAGAAACTTCTGGGACCCCACGTGGAGGGCCTGAA 1769
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  1830 GGACACGCTGGGGCTGGGGCTACAGGGCGGCATCCCCAACGGCTACCTGGTCCTAGACCT 1889
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                                                                                                     GGCGGAGGAGCGGCACCGCCCGGTGCGGGACTGGATCCTACGGCAGCGGCAGGACGACCT 1829
                                                                                                                                                    GCAGCCGTTGACTGTGGCTGAGGTGCAGAAACTTCTGGGACCCCACGTGGAGGGCCTGAA 21369
                                                                                                                                                                                                                                                          Conservative
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/note="3
                                                                                                                                                                                                                                                                                                                                                         /note="CpG island"
/evidence=not_experimental
20410. .21099
/note="15 copies 46 mer 67% conserved"
20436. .21077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note-"Tandem repeat. Forced join. Restriction digest data (ECORI, HINCII, SACI) suggest 400 bases are missing." complement(16716. .17130) /note-"match: GSS: Em:AQ187418" 17850. .18744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QQEAARAALQGGGFPYGFPSTWSVSTMDALRGLLPVLGQPIIRSIPQGIVAAWRQRSS
RDPSWRQPERTILRPREREVEKTACPSGKKAREIDESIIFYKWSELDACUDAALLAT
QMDRVNAIPETYEQLDVLKHKLDELYPQGYPESVIQHLGYLFLKWSPEDIRKWNVTSL
ETLKALLEVNKGHEMSPQAPRRPLPQVATLIDREVKGRQQLDKDTLDTLTAFYBCYLC
SLSPEELSSVPPSSIWAVRPQDLDTCDPRQLDVLYPKARLAFQNMNGSEYFVKIQSFL
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CLAHRLSEPPEDLDALPLDLLLFLNPDAFSGPQACTRFFSRITKANVDLLPRGAPERQ
RLLPAALACWGVRGSLLSEADVRALGGLACDLPGRFVAESAEVLLPRLVSCPGPLDQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="CAC37289.1"
/bxotein_id="CAC37289.1"
/bxref="GI:13751645"
/ranclatic="""
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/note="MIR repeat: matches 103. .191 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VRDWILRQRQDDLDTLGLGLQGGIPNGYLVLDLSMQEALSGTPCLLGPGPVLTVLALI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /evidence=not_experimental
/product="C335H7.1 (mesoth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       )oin(15616 .15700,16168 .16211,16577 .16626,16598
1/582 .17661,17842 .17971,18045 .48238,18462 .185
18626 .18725,18944 .19172,19270 .19425,19579 .197
19820 .19947,20311 .20405,21314 .21500,21583 .216
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/product="C335H7.1 (mesothelin)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="MSLN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ]oin(15529..15700,16168..16211,16577..16626,16958..1
[7582..17661,17842..17971,18045..18238,18462..18552,
18626..18725,18994..19172,19270..19425,19579..19745,
19820..19947,20311..20405,21314..21500,21583..21800)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /evidence≖not_experimental
L8858. .18989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'gene="MSLN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="MIR repeat: matches 21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note="CpG island"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'gene="MSLN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        translation="MALPTARPLLGSCGTPALGSLLFLLFSLGWVQPSRTLAGETGQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="match: proteins: Tr:Q61468 Tr:Q14859"
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                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                       Score 307.6; DB 9
Pred. No. 1.9e-45;
0; Mismatches 4
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                                                                                                                                                                                                                                                                                                            DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .147 of consensus
                                                                                                                                                                                                                                                                                                       Length 37307;
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                                                                                      COMMENT
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TITLE
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                                                                                                                                                                         TITLE
                                                                                                                                         JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21490 CAGCATGCAAGGTGGGCGGGCGGCCAGGGCCAGGGCTGGGGGCAGAGCTGGGGGCGTGGA
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                                                                                                                                                                               RS Birren, B. Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Boguslavkiy, L., Boukhġalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Domino, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-plerre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Grand-plerre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Grand-plerre, N., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., Mcheeters, R., Meldrim, J., Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivar, J., Naymond, C., Riley, R., Rogov, P., Rothman, D., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Voung, G., Zalnoun, J., Zimmer, A., and Zody, M., X., Wyman, D., Ye, W.J., Direct, Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGCAGACA 21797
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 154616)
Birren, B., Linton, L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AC067772
AC067772.2 GI:8099942
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                         All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                      Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens, clone RP11-728H8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalla;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HTG; HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 154616)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                154616 bp DNA HTG ZOTH
ns clone RP11-728H8, WORKING DRAFT SEQUENCE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nusbaum,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .C. and Lander, E.
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NOTE: This is a 'working draft' sequence. It currently consists of 24 contigs. The true order of the pleces is not known and their order in this sequence record is arbitrary, Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
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Insert size: 152316; sum-of-contigs
Quality coverage: 3.8 in Q20 bases; agarose-fp
Quality coverage: 4.6 in Q20 bases; sum-of-contigs
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48226 48325: gap of 100 bp
48326 54012: contig of 5687 bp in 1.
54013 54112: gap of 100 bp
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71779: gap of 100 bp
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96350: contig of 10712 bp in length
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71780. .77756
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54113. .61592
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21307. .24213
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48326. .54012
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/db_xref="taxon:9606"
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11157797
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence, structure and pathology of the fully annotated Mb of the short arm of human chromosome 16 hum. Mol. Genet. 10 (4), 339-352 (2001)
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Homo sapiens 16915.3 sequence
AE006464 AE005175
AE006464.1 GI:14336700
                                                                                                                                                                                                                                                                                                   Submitted (07-DEC-2000) MRC Molecular Haematology Unit, Weatherall Institute of Molecular Medicine, John Radcliffe Hospital, Oxford,
                                                                                                                                                                                                                                                                                                                                                                              Daniels,R.J.,
Tufarelli,C.,
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Mammalia;
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nniels,R.J., Peden,J.F.,
sfarelli,C., Kearney,L.,
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                                                                                                   23/10/2000"
                                                                                                                 note="GC_rich;
                                                                                                                                                         /map="16p13.3"
                                                                                                                                                                                                                                                            Location/Qualifiers
sapiens"
                                                                                                                     RepeatMasker predicted
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Buckle,V.J., Doggett,N.A., Flint,J.
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of 8.
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2478. .2582
/note="L2; RepeatMackor -----
                                                                                                                                                 /rpt_family="SINE/Alu"
complement(13829. .14055)
note="LIMB8; RepeatMasker predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                  /rpt_family="SINE/Alu"
5174. .5490
/note="Alusx; RepeatMasker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="AluSx; RepeatMasker
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/evidence=not_experimental
42. 100
   complement(14808. .14991)
/note="AluJb; RepeatMasker predicted
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                                                                                                                                                                                                                                               /rpt_family="DNA/MER1_type"
complement(11229. .11378)
                                                                                                                                                                                                                                                                                                                        /rpt_family="SINE/Alu"
complement(10481. .10623)
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                                        /rpt_family="LINE/L1"
                                                                                                                                      23/10/2000"
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                                                                                                                                                                                                                                                                                                                                                                                              /rpt_family="SINE/Alu"
complement(8662. .8958)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="cosmid 366d1"
                                                                          note="L1MB8; RepeatMasker predicted"
                                                                                                                                                                                                                            /note="AluJo; RepeatMasker predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1805. .5105
/note="AluY; RepeatMasker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /rpt_family="SINE/Alu"
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/note="AluSx; RepeatMasker
                                                                                                             rpt_family="LINE/L1"
                                                                                                                                                                                                                                                                                                                                                                           note="AluSg; RepeatMasker predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3658. .39964
/note="HS366D1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="FRAM; RepeatMasker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rpt_family-"LINE/L2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="GC_rich; RepeatMasker predicted
23/10/2000"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'gene="SOLH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                   note="MER58; RepeatMasker predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="GC_rich; RepeatMasker predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rpt_family="SINE/Alu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="Similar to Unigene cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rpt_family="SINE/Alu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                oue="L2; RepeatMasker predicted/10/2000"
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29. 21437,21524. 21707,21851. 22074,23538. 23663,
18. 23900,24287. 24448,24537. 24766,24841. 25007,
39. 25277,25575. 26868)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .46058
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /rpt_family="Low_complexity" 34647. .34860
                                                                                                                                                 /rpt_family="Low_complexity"
32807. .32836
/note="GC_rich; RepeatMasker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /rpt_family="Simple_repeat"
17340 .17414
/note="AluJb; RepeatMasker predicted
23/10/2000"
                                                                                               /rpt_family="Low_complexity"
32937. .33018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /rpt_family="SINE/Alu"
15007. .15301
note="Alusx; RepeatMasker predicted
3464/. .34860
/note="(CA)n; RepeatMasker predicted
                                                                                                                              rnote="GC_rich; RepeatMasker predicted
23/10/2000"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JVILSQLEGNAGESITHRLAHRKAAQAFLSDWTASKGTHSPPLTPEVAGLHGPRPL"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="matvgewSCVRCTFLNPAGQRQCSICEAPRHKPDLNHILRLSVE
EQKWPCARCTFRNFLGKEACEVCGFTPEPAPGAAFLPVLNGVLPKPPAILGEPKGSCQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'product="small optic lobes homolog"
'proteln_id="AAK61233.1"
'db_xref="g1:14336701"
'db_xref="MIM:603267"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'gene="SOLH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                join(19075. .20523.21229. .21437,21524. .21707,21851. .2
23538. .23663,23748. .23900,24287. .24448,24537. .24766,
24841. .25007,25099. .25277,25575. .25752)
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/note="AluJb; RepeatMasker
23/10/2000"
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                                                                      note="GC_rich; RepeatMasker predicted
                                                                                                                                                                                                          'note="G-rich; RepeatMasker predicted
13/10/2000"
                                                                                                                                                                                                                                                            'evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'db_xref="SPTREMBL:075808"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .6939. .17110
'note="(CCTCG)n; RepeatMasker predicted
                                                                                                                                                                                                                                                                               note="CpG island; i+E69ncorporates tandem repeat; RJD1"
                                                                                                                                                                                                                                                                                                                                                                                                                9443. .19488
'note="(GGA)n; RepeatMasker
3/10/2000"
                                                                                                                                                                                                                                                                                                                                                        note="C-rich; RepeatMasker predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  codon_start=]
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(19075. .20523.212)
                                                                                                                                                                                                                                                                                                                                                                                           family="Simple_repeat"
                                                                                                                                                                                                                                                                                                                    family="Low_complexity"
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REFERENCE
AUTHORS
TITLE
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KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                         RESULT 15
AC092381/c
                                                                                                                                                                                                                                                                                                                          DEFINITION
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241088
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGTGGGCGCTCTGAGTCACCCCTCTCTCTGTAGAGGCCCTCTCGGGGACGCCCTGCCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGACACGCTGGGGCCTACAGGGCGGCATCCCCCAACGGCTACCTGGTCCTAGACCT 1889
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGCAGACA 241095
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACGGGTGGTCCCCGTTCCACCCCAAGAGAACTCGCGCTCAGTAAACGGGAACATGCCCCC
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Eukaryota; Metazoa; Chordata; Cr
Mammalia; Eutheria; Primates; Ca
1 (bases 1 to 155770)
DOE Joint Genome Institute.
Sequencing of Human Chromosome 1
Unpublished
                                                                                                                                                                                                                                                                                      Homo sapie
SEQUENCE,
                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                          AC092381.1 GI:14589570
                                                                                                                                                                                                              HTG; HTGS_PHASE1; HTGS_DRAFT
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ENCE, 23 unordered p
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complement(35112. .35278)
note="MER53; RepeatMasker predicted"
22/20/2007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        homology support for exon1"
35531. .41726
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/gene="RJD1"
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* NOTE: This is a 'working draft' sequence. It currently consists of 23 contigs. The true order of the pieces is not known and their order in this sequence record is
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Submitted (03-JUL-2001) Production Sequencing Facility, DOE Joint Senome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center: Joint Genome Institute Center Code: JGI
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/db_xref="taxon:9606"
/chromosome="16"
/clone="RPCI human BAC library 11"
/clone_1lb="RPCI human BAC library 12"
29940 a 45687 c 45637 g 32240 t 2266 others.
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05770: contig of 21711 bp in length.
100cation/Qualifiers
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               2001, 11:24:02
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Listing first 45 summaries
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| SIDSZ/gcgdata/geneseq/geneseqn/NA1980_DAT:*
| SIDSZ/gcgdata/geneseq/geneseqn/NA1981_DAT:*
| SIDSZ/gcgdata/geneseq/geneseqn/NA1981_DAT:*
| SIDSZ/gcgdata/geneseq/geneseqn/NA1981_DAT:*
| SIDSZ/gcgdata/geneseq/geneseqn/NA1984_DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Key CDS

Location/Qualifiers

sig_peptide

2 1992.4 93.2 3 992.8 46.4 4 983.8 46.0 5 871.4 40.8 6 219.8 10.3 7 197 9.2 8 150.2 7.0 9 130.8 6.1 10 89.8 4.2 11 75 3.5	Result Query No. Score Match Length DB
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15 21 21 22 22 22 23 15 15	.
AAQ63972 AAA64366 AAA64362 AAA64363 AAF94935 AAQ63971 AAH81882 AAQ70028 AAA70028 AAA770028	ID AAT91079
Megakaryoctye pote Soluble mesothelin related Mesothelin related Human ovarian canc Meg-Pot fragment. Rat differential t Human ovarian carc Human gene signatu Meg-Pot fragment.	Description Human CAK1 antigen

polyA_signal

/*tag= a
145..195
/*tag= b
/note= "putative signal sequence for membrane
insertion"

/note= "variant polyadenylation signal"

05-JAN-1996; 03-JAN-1997; 17-JUL-1997. W09725068-A2

96US-0010166 97WO-US00224.

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<pre>tumour specific antigen; cell cancer; gene therapy;</pre>	in) cDNA.			8 BP.		ALIGNMENTS	AA136333	1400	AAHLB319	AAA29349	AAA59553	AAX15650	AACO1/31	AAZ22248	AAV21683	AAX90923 AAX23778	AAA75454	AAF82902	AAA50254	AAV55831	AAC / 8.1.5 /	AAC95555	AAV62138	AAA10594	AAA09686	AAX90924	AAC76736	AAD08215	AAA53800	AAT12168	AAZ49952	AAA1.0594	534	349	AAT:25748
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This cDNA clone codes for CAK1 antigen (see AAW26674) which is found on mesothelium, mesotheliumas, ovarian cancers and some squamous cell carcinomas. The antigen has been designated mesothelin. The clone was isolated from a HeLa S3 cDNA library by
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                                                                                                                                             GGAGTCCTGACAACCCCCCATAACATTTCCAGCCTCTCCCCCTCGCCAACTCCTTGGCTTC
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gcacagaagaatgtcaagctctcaacagagcagctgcgctgtctggctcaccggctctct
               GCACAGAAGAATGTCAAGCTCTCAACAGAGCAGCTGCGCTGTCTGGCCTCACCGGCTCTCT
                                                                CCGTGTGCGGAGGTGTCCGGCCTGAGCACGGAGCGTGTCCGGGAGCTGGCCTGTGGCCTTG
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11-NOV-1992;
09-DEC-1992;
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92JP-0301387.
92JP-0329546.
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                                               acggatgcggtgccgttgactgtggctgaggtgcagaaacttctgggaccccacgtg
                                                              ACGGATGCGGTGCCGTTGACTGTGGCTGAGGTGCAGAAACTTCTGGGACCCCACGTG
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1450
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTCCGGCGGAAGTGGAGAAGACAGCCTGTCCTTCAGGCAAGAAGGCCCGCGAGATAGAC 1029
                                                                                                                                                                                                                                                        CTGGACACGTGTGACCCAAGGCAGCTGGACGTCCTCTATCCCAAGGCCCGCCTTGCTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                             AGCCCCGAGGAGCTGAGCTCCGTGCCCCCCAGCAGCATCTGGGCGGTCAGGCCCCAGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAGACCCTGAAGGCTTTGCTTGAAGTCGACAAAGGGCACGAAATGAGTCCTCAGGCTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          aagcataaactggatgagctctacccacaaggttaccccgagtctgtgatccagcacctg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gccacccagatggaccgcgtgaacgccatccccttcacctacgagcagctggacgtccta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCCACCCAGATGGACCGCGTGAACGCCATCCCCTTCACCTACGAGCAGCTGGGACGTCCTA 1149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAGAGCCTCATCTTCTACAAGAAGTGGGAGCTGGAAGCCTGCGTGGATGCGGCCCTGCTG
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CCCCACGTGGAGGGCCTGAAGGCGGAGGAGCGCCACCGCCCGGTGCGGGACTGGATCCTA
                                                                 AAGCTGCGGACGGATGCGGTGCCGGTTGACTGTGGCTGAGGTGCAGAAACTTCTGGGA 1749
                                                                                                                                                                                    ACGGAGGATTTGAAGGCGCTCAGTCAGCAGAATGTGAGCATGGACTTGGCCACGTTCATG
                                                                                                                                                                                                                                                                                                                             ctggacacgtgtgacccaaggcagctggacgtcctctatcccaaggcccgccttgctttc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGGCGGCCCTCCCACAGGTGGCCACCCTGATCGACCGCTTTGTGAAGGGAAGGGGCCAG 1389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gagaccctgaaggctttgcttgaagtcaacaaagggcacgaaatgagtcct------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ggctacctcttcctcaagatgagccctgaggacattcgcaagtggaatgtgacgtccctg
                                           aagctgcggacggatgcggtgccgttgactgtggctgaggtgcagaaacttctggga
                                                                                                                                                                                                                                Conservative
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97.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 871.4;
Pred. No. 1.
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..8e-163;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       These can be used in the diagnosis, treatment and prevention of cancer, optionally by gene therapy or in the form of a vaccine. present sequence is an example of one of these sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-SEP-1999; 99US-0394374.
01-MAY-2000; 2000US-0561778.
15-AUG-2000; 2000US-0640173.
07-SEP-2000; 2000US-0656668
                                                                                                                                                                                                                                                                       1243 ATTCGCAAGTGGAATGTGACGTCCCTGGAGACCCTGAAGGCTTTGCTTGAAGTCGACAAA 1302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 396 BP; 77 A; 139 C; 111 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isolated polypeptides associated with ovarian carcinomas, nucleic acids that encode them, useful for the prevention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xu J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      treatment of ovarian cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-MAR-2001.
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                                                                                                                                                                                                                                                                                                                                 Local Similarity
nes 279; Conserv
                                                                                                                                                                                                                      æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           present invention provides a number of coding sequences and proteins over-expression of which is associated with ovarian carcinoma/cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6
                       GACCGCTTTGTGAAGGGAAGGGGCCAGCTAGACAAAGACACCCTAGACACCCCTGACCGCC
                                                                                                                                     GGGCACGAAATGAGTCCTCAGGCTCCTCGGCGGCCCCTCCCACAGGTGGCCACCCTGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGCTACCTGGTCCTAGACCTCAGCGTGCAAG
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                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cancer; vaccine; gene therapy; carcinoma; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         189pp;
                                                                                                                                                                                                                                                                                                                                                     10.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               English
                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                        Score 219.8; DB 2
Pred. No. 9.3e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ΒP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                           396;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     proteins,
                                                                                                                                                                                                                                                                                                                                    Gaps
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RESULT AAQ63971 ID AAQ63971 AAQ63971 AAQ63971 OR-IT OR
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                                                                         밁
                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-OCT-1992;
11-NOV-1992;
09-DEC-1992;
                                                                                                                                                                                                                                                                                                                                            Use of the primers given in AAQ77809-10 in PCR resulted fragments given in AAQ63971.
DNA encoding Meg-Pot has potential use in treatment of thrombocytopenia and low platelet function.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Megakaryoctye potentiator; Meg-Pot; thrombocytopenia; platelet; amplification; primer; polymerase chain rea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1543
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                                                                                                                                                                                                                                                                                              Sequence 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 51; 74pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-MAY-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAQ63971 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   thrombocytopenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New mega:karyoctye potentiator -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hattori K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-OCT-1993;
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DB; AAR53991.
                                                                                                                       AACTCCTTGGCTTCCCGTGTGCGGAGGTGTCCGGCCTGAGCACGGAGCGTGTCCGGGAGC 346
                         TGGCTGTGGCCTTGGCACAGAAGAATGTCAAGCTCTCAACAGAGCAGCTGCGCTGTCTGG
                                                                    aactccttggcttcccgtgtgcggaggtgtccggcctgagcacggagcgtgtccgggagc
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197;
                                                                                                                                                                                              Similarity
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                                                                                                                                                                       llarity 100.0%;
Conservative 0;
                                                                                                                                                                                                                                                                                                 BP;
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92JP-0301387.
92JP-0329546.
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                                                                                                                                                                                                                                                                                                 32 A;
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                                                                                                                                                                                                                       9.28;
                                                                                                                                                                                                                                                                                              66 C; 59 G;
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                                                                                                                                                                       DB 15;
2.7e-30;
hes 0;
                                                                                                                                                                                                                  Length 197;
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1082 CCCTGCTGGCCACCCAGATGGACCGCGTGAACGCCATCCCCTTCACCTACGAGCAGCTGG 1141

ccctgctggccggccagatggaccttgtgaatgaaattccctttacctacgagcagctca

61

Query Match Best Local Similarity

7.0%;

Score 150.2; Db ... Pred. No. 4.9e-21; Pred. No. 489-21;

Indels

Gaps

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Length

255;

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                          suppressor genes. (I), and polypeptides encoded by them, are useful as targets for diagnosis or therapy and in screening to determine the effects of an active compound (potential pharmaceutical) on a cell line, particularly for diagnosis and treatment of tumors, especially by modulating expression of (I) (by gene therapy, antisense RNA or ribozyme methods) or by modulating the amount and/or location of (I)-encoded polypeptides (by administration of the polypeptide or its activator, antibody (optionally as a conjugate) or inhibitor). The method allows identification of many class II tumour suppressor genes (i.e. genes that are not primary targets for tumour initiating mutations). AAH81492-AAH82376 represent the human and rat derived nucleic acid fragments described in the method of the invention.
                                                                                                                                                                                                                     This invention describes a nucleic acid (I) with differential expression between tumour and normal cells and which has cytostatic activity. (I) work as modulators of Ras activity by inducing expression of tumour
                                                                                                                                                                                                                                                                                                                                  Nucleic acids differentially expressed between tumor and normal cells, useful for diagnosis or therapy of tumors and for screening active
                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-483415/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Differential transcription; human; rat; tumour cell; cytostatic; Ras modulator; Class II tumour suppressor gene; gene therapy; ss
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Sequence 255 BP; 71 A; 71 C;
                                                                                                                                                                                                                                                                                      Claim 6; Page 488; 579pp;
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Grips M, Hellriegel M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-JAN-2001; 2001WO-EP01003
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Sers C;
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  Query Match
Best Local Similarity
Matches 182; Conserv
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17-DEC-1998;
23-JUN-1999;
                                                                                                                                                                                                      The present invention describes an isolated polypeptide comprising an immunogenic portion of an ovarian carcinoma protein (or its variants). Ovarian carcinoma proteins, and polynucleotides encoding them, have cytostatic activity and can be used in gene therapy and vaccines. Ovarian carcinoma polypeptides, nucleic acids, antibodies and vaccines are useful for the prevention, diagnosis and treatment of cancer, preferably ovarian cancer. AAA69691 to AAA70077 and AAB12552 to AAB12557 represent human ovarian carcinoma polypucleotides and proteins used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immunogenic portion of an ovarian carcinoma acid encoding it, useful for the diagnosis, cancer, preferably ovarian cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; ovarian carcinoma; ovarian cancer; therapy; diagnosis; tumour antigen; identification; cytostatic; gene therapy; vaccine;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 18; Page 182; 299pp; English.
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                                                                                                                                                                                   exemplification of the present invention.
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99US-0338933.
99US-0404879.
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XX AT2
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                                                                                       A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "GS" sequences given in AAT19001-T26837 and which is able to hybridise to part of human genomic DNA, CDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-en untranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as means of diagnosing abnormal cell function or for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Identifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gene signature; messenger RNA; mRNA; relative abundance; human; cloning; mapping; non-biased library; diagnosis; cell typing; abnormal cell function; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 1902; 2245pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1995-206931/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MATS/) MATSUBARA K. (OKUB/) OKUBO K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9514772-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAT25668 standard; cDNA to mRNA: 95
                                                                recognising different cell types
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matsubara K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCTTCACCTACGAGCAGCTGGACGTCCTAAAGCATAAACTGGATGAGCTC-TACCCACAA 1179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GNNCATTCGCAAGTGGAAATGTGNCGTCCTTGNAGACCNTGAAGGNCTTTGCTTGAAGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGACATTCGCAAGTGG-AATGTGACGTCCCTGGAGACCCCTGAAGG-CTTTTGCTTGAAGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93JP-0355504.
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detection;
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Sequence

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RESULT 11
AAQ63970
ID AAQ639
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XX Meg-Po
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KW Platel
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PN WO9410
XX HOMO S
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Best Local Similarity
""" hes 75; Conserve
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Best Local Sim
Matches 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-OCT-1992;
11-NOV-1992;
09-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Megakaryoctye potentiator; Meg-Pot; thrombocytopenia;
platelet; amplification; primer; polymerase chain reaction;
                                                                                                                                                                                                                                                                 Sequence 75 BP; 11 A; 31 C; 16 G; 17 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1994-167467/20.
P-PSDB; AAR53990.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2083 GCTCAGTAAACGGGAACATGCCCCCTGCAGACAAA 2117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2023 GATCCCCGCCTGGCCAGGAGCAGGCACGGGTGATCCCCCGTTCCACCCCAAGAGAACTCGC 2082
                                                                                                                                                                                                                                                                                                  thrombocytopenia and
                                                                                                                                                                                                                                                                                                                                 Use of the primers given in AAQ77805-08 in PCR resulted fragments given in AAQ63969-70.
                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 50; 74pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                           New mega:karyoctye potentiator -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hattori K, Kojima T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-MAY-1994.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAQ63970 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                   thrombocytopenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CHUS ) CHUGAI SEIYAKU KK.
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                                                415
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 12
                                                                                                                                                                                                                                                                                                                   encoding Meg-Pot
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gctcagtaaacgggaacatgccccctgcagccaaa
                                                                                                                 ctctctgagccccccgaggacctggacgccctcccattggacctgctgctattcctcaac
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                                                                                                                                                                                    Conservative
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92JP-0301387.
92JP-0329546.
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                                                                                                                                                                                                 3.5%;
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                                                                                                                                                                                                                                                                                                has potential use in treatment of low platelet function.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oh-eda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP
                                                                                                                                                                                    0;
                                                                                                                                                                                                 Score 75;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 89.8; DB 16;
Pred. No. 3.6e-09;
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                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                 for potential treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yamaguchi
                                                                                                                                                                                DB 15; L
2.9e-06;
hes 0;
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                                                                                                                                                                                                                 Length 75;
                                                                                                                                                                                  Indels
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AAT2574
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KW human;
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Best Local Similarity
Matches 69; Conserv
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11-NOV-1992;
09-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1994-167467/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-DEC-1994 (first entry)
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                                                                                                                                                   10-OCT-1996 (first entry)
                                                                                                                                                                                                                 AAT25748 standard; cDNA to mRNA; 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 69 BP; 7 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hattori K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-OCT-1993;
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                 Homo sapiens
                                                                                                                   Human gene signature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  thrombocytopenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   thrombocytopenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New mega:karyoctye
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CHUS ) CHUGAI SEIYAKU
                                                                                                                                                                                                                                                                                                                                  343 GAGCTGGCT 351
                                                                                                                                                                                                                                                                                                  61 gagctggct 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kojima T,
                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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92JP-0301387.
92JP-0329546.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
                                                                                                                   HUMGS07964.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74pp; Japanese.
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Gene signature; messenger RNA; mRNA; relative abundance; human; cloning; mapping; non-biased library; diagnosis; cell typing; abnormal cell function; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Use of the primers given in AAQ77805-08 in PCR resulted fragments given in AAQ63969-70.
DNA encoding Meg-Pot has potential use in treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Megakaryoctye potentiator; Meg-Pot; thrombocytopenia;
platelet; amplification; primer; polymerase chain reaction;
                                                                                                                                                                                                                                                                                                                                                                    -Pot has potential use in treatment and low platelet function.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22 C; 26 G; 14 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 69; DB 15; Le
;; Pred. No. 4.4e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for potential treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yamaguchi N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                        frequency;
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                                                                                                                                                                                                                                                                                                 AAX53491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A single-stranded DNA (or its complementary strand or the corresp. C double-stranded DNA) which comprises one of the 7837 "GS" sequences given in AAT19001-T26837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'- untranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                        2054 GATCCCCGTTCCACCCCAAGAGAACTCGCGCCTCAGTAAACGGGAACATGCCCCCTGCAGA 2113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 1920;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tissues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Identifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. \tt mRNA in specific human
              chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma; colon cancer; breast cancer; lung cancer; pancreatic cancer;
                                                respiratory distress syndrome; pain; cystic fibrosis; pulmonary hypertension; pulmonary vasoconstriction; emphysema
                                                                                                     impaired respiration; inflammation; lung disease;
pulmonary vasoconstriction; inflammation; allergic rhinitis;
                                                                                                                                                                        Human adenosine Al receptor antisense oligonucleotide fragment.
                                                                                                                                                                                                            05-JUL-1999
                                                                                                                                                                                                                                              AAX53491;
                                                                                                                                                                                                                                                                              AAX53491 standard; DNA; 114955
                                                                                                                                                                                                                                                                                                                                                                                                    2114 CAAAAAAA 2121
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                                                                                   acute asthma; allergy; asthma; impeded respiration;
                                                                                                                                   Antisense oligonucleotide; multiple target; antisense treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 68 BP; 21.A; 23 C; 14 G; 9 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matsubara K, Okubo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MATS/) MATSUBARA K. (OKUB/) OKUBO K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                recognising different cell types.
                                                                                                                                                                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                          (first entry)
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Pred.
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No. 0.002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5;
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hepatic metastasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68
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                                                                                                                                                                                                                                                                                                                                 Db 104261 ggccgsnnndnnccgcbggccbgggcgcgccgccggccgg--gccsnnndnnccgcbggc 104318
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Best Local Similarity
    104499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antisense treatment of diseases and conditions. Typical diseases and conditions are those associated with impaired respiration and inflammation, including lung diseases, pulmonary vasoconstriction, inflammation, altergic rhinitis, acute asthma, altergies, asthma, impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, pulmonary hypertension, pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g. colon cancer, breast cancer, lung cancer, pancreatic cancer, hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastasses, as well as all types of cancers which may metastasize or have metastasized to the lungs, including breast and prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            non-coding regions of RNAs corresponding to target genes, gene initiation codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'-end and the juxta-section between coding and non-coding regions and all segments of RNAs encoding proteins associated with one or more diseases, conditions or mixtures. The antisense oligonucleotides may be derived from sequences AAX55272-74. These multiple target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 114955 BP; 6071 A; 29417 C; 36712 G; 21328 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        oligonucleotides (specifically AAX55180-271) can be used for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         directed against at least 2 mRNAs selected
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The specification describes antisense oligonucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 37; 120pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-JUN-1998;
17-SEP-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New antisense oligonucleotides used in treatment of, e.g. pulmonary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (UYEC-) UNIV
                                                                                                                                                                                                                                                                                          73
                                                                                                                                                                                                                                                                                                                                                                            13 GGCCGGCCACTCCCGTCTGCTGTGACGCGCGCGACAGAGAGCTACCGGTGGACCCACGGTG 72
cgcgccgccggcsnnndnnccgcbsggccbgggcgcgccgccgsnnndnnccgcbggccb
                                        ACCCCCCATAACATTTCCAGCCTCTCCCCTCGCCAACTCCTTGGCTTCCCCGTGTGCGGAG 312
                                                                               ccggccgsnnndnnccgcbggccbaggcgcgcgcgnnndnnccgcbggccbggg
                                                                                                                          GCGAGGACCCTGGCTGGAGAGACAGGGACGGAGTCTGCCCCCCTGGGGGGGAGTCCTGACA 252
                                                                                                                                                               nndnnccgcbggccbgggcgcgcccgccggcnnndnnccgcbggccbgggcgcgccg
                                                                                                                                                                                                      TGTGGGGACCGCCTGGCAGCCTCCTGTTCCTGCTCTTCAGCCTCGGATGGGTGCATCCC 192
                                                                                                                                                                                                                                               cbgggcgcgccgccggccgggcsnnndnnocgcbggccbgggcgcgccgccggccgggsn 104378
                                                                                                                                                                                                                                                                                          CCTCCCTCCCTGGGATCTACACAGACCATGGCCTTGCAACGGCTCGACCCCTGTTGGTCC 132
                                                                                                                                                                                                                                                                                                                                                                                                                     300;
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97US-0059160
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                                                                                                                                                                                                                                                                                                                                                                                                                                        31.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                   97;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 58.6; DB Pred. No. 0.017;
                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                     557;
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RESULT 15
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                                                                                                                                                                                           pulmonary hypertension; pulmonary vasoconstriction; emphysema;
chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
colon cancer; breast cancer; lung cancer; pancreatic cancer;
                                                                                                                                                                                                                                                                      impaired respiration; inflammation; lung disease;
pulmonary vasoconstriction; inflammation; allergic rhinitis;
acute asthma; allergy; asthma; impeded respiration;
                                                                                                                                                                                                                                                   acute asthma; allergy; asthma; impeded respiration; respiratory distress syndrome; pain; cystic fibrosis;
                                                                                                                           Synthetic
                                                                                                                                                                 prostate cancer; ss
                                                                                                                                                                                  hepatocellular carcinoma; kidney
                                                                                                                                                                                                                                                                                                                           Antisense oligonucleotide; multiple target; antisense treatment;
                                                                                                                                                                                                                                                                                                                                                              Human adenosine Al receptor antisense oligonucleotide fragment.
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                17-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAX53491 standard; DNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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17-SEP-1997;
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GCCCVNNHNNNSCGGCCCGGCCGCGCGCCCVGNNHNNNSCGGCCCGGCCGGCCGGCG
                                                 ACCTGCTGCTATTCCTCAACCCAGATGCGTTCTCGGGGGCCCCAGGCCTGCACCCGTTTCT
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Search completed: December 7, 2001, 10:44:45 Job time: 2642 sec

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Sequence 17, Appl	17,	Sequence 1, Appli	Sequence 1, Appli	ω,	u '	Sequence 4, Appli	Sequence 2, Appli	Sequence 1, Appli	Sequence 2, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 22, Appl	Sequence 21, Appl	Sequence 7, Appli	Sequence 7, Appli	Sequence 7, Appli	

ALIGNMENTS

US/08776271

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PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/00224
FILING DATE: 03-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/010,156
APPLICATION NUMBER: US 60/010,156
ATTORNEY/AGENT INFORMATION:
NAME: Faris, Susan K.
REGISTRATION NUMBER: 41,739
REGISTRATION NUMBER: 41,739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, \
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,271
FILING DATE: 01-DEC-1998
CLASSIFICATION: 424
                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
                                                 MOLECULE TYPE: cDNA FEATURE:
                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 2138 base pair
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TITLE OF INVENTION: Present on Mesothelium, Mesotheliomas and Ovarian Cancers
TITLE OF INVENTION: and Methods and Kits for Targeting the Antigen
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NAME/KEY:
LOCATION:
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STATE: California
                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: sing
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      AGCAGGCACGGGTGATCCCCCGTTCCACCCCCAAGAGAACTCGCGCTCAGTAAACGGGAACA
                                GCCTGAGGGCCCCACTCCCTTGCTGGCCCCCAGCCCTGCTGGGGATCCCCGCCTGGCCAGG
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REFERENCE/DOCKET NUMBER: 0152
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                         Query Match
Best Local Similarity
Matches 2138; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/215,035
FILING DATE: NO. 6153430 yet assign
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/776,271
FRIOR APPLICATION NUMBER: US 08/776,271
FRIOR DATE: 01-DEC-1998
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APPLICANT: Chang, Kai
TITLE OF INVENTION: Met
TITLE OF INVENTION: Pri
TITLE OF INVENTION: An
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APPLICATION NUMBER: WO PCT
FILING DATE: 03-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/
FILING DATE: 05-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: FAILS, SUSAN K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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CORRESPONDENCE ADDRESS:
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CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                          LENGTH: 2138 base portion of the TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear
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AGGAATTCCGGTGGCCGGCCACTCCCGTCTGCTGACGCGCGGACAGAGAGCTACCGGT
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linear
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Present on Mesothelium, Mesotheliomas and Ovarian Cancers
and Methods and Kits for Targeting the Antigen
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Yamaguchi, No. 5
Kojima, Tetsuo
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NAME: MUTPHY Jr., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 230-107P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 2129 base pairs
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Best Local Similarity
Matches 2075; Conserv
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HYPOTHETICAL: NO
IMMEDIATE SOURCE:
CLONE: pKP027
FEATURE:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
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CORRESPONDENCE ADDRESS:
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Sequence 32, Application Patent No. 5723318 GENERAL INFORMATION: Yamagu STREET: P.O. Box 747
CITY: Falls Church
STATE: Virginia
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE APPLICANT: Hattori, Kun
TITLE OF INVENTION: GenTITLE OF INVENTION: PotNUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS: ADDRESSEE: Birch, St. STREET: P.O. Box 747 Kojima, Tetsuo Oh-Eda, Masayoshi Yamaguchi, No. compatible Genes Coding Potentiator Stewart, Kunihiro 37 US/08426819A 5723318omi Kolasch for Megakaryocyte Birch

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US-08-426-819A-31
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Best Local :
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SEQUENCE CHARACTERISTICS:
SEQUENCE 197 base pairs
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Yamaguchi, No. 57:
APPLICANT: Kojima, Tetsuo
APPLICANT: Oh-Eda, Masayoshi
APPLICANT: Hattori, Kunihiro
                                                                                                                                                                    NUMBER OF SEQUENCES: 3:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Sto
                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Genes Coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
COMPUTER READABLE FORM:
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OTHER INFORMATION:
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                                                                                                CITY: Falls Church
STATE: Virginia
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SOFTWARE: Patentl
                                                                COUNTRY:
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                                   22040-0747
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/note- "amplified product from pool D using primers 3AS1 and
7SA1"
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Best Local Similarity
Matches 75; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 230-107P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release*#1.0.
CURRENT APPLICATION DATA:
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 230-107P
TELECOMMUNICATION INFORMATION:
                                                     ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald M.
                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Hattori, Kunihiro TITLE OF INVENTION: Genes Codin TITLE OF INVENTION: Potentiator
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                                                                                          APPLICATION NUMBER: US/08/426,819A FILING DATE: 21-APR-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                 ADDRESSEE: Birch, Stewart, Kolasch & Birch
STREET: P.O. Box 747
CITY: Falls Church
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE: 21-AP
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Oh-Eda, Masayoshi
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                                                                                                                                                                     Version #1.30
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US-08-253-155A-7
; Sequence 7, Application US/08253155A
; Patent No. 5691147
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                                                                                                                                 US-08-253-155A-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 3.2%;
Best Local Similarity 100.0%;
Matches 69; Conservative
                                                               Query Match
Best Local
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APPLICANT: Gyuris, Jeno
APPLICANT: Draetta, Giulio
TITLE OF INVENTION: CDK4 Binding Proteins
                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS:DOS
SOFTWARE: ASCIT(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/253,155A
FILING DATE: 02-JUN-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: VINCENT MATTER: D
                                                                                                                                                                                                                                           TELEFAX: (617) 227-594
INFORMATION FOR SEQ ID NO:
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TOPOLOGY: not
MOLECULE TYPE:
                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MITTELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEPAX: (617) 227-5941
                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 3407 base pairs
                                                                                                                                               TOPOLOGY: 11
MOLECULE TYPE:
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: LAHIVE & COCKFIELD
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                 945 TGAACGGACCATCCTCCGGCCGCGTTCCGGCGGGAAGTGGAGAAGACAGCCTGTCCTTC 1004
                                              y Match 2.5%;
Local Similarity 46.4%;
hes 170; Conservative
                                                                                                                                                                                                                                                                                                                             NAME: Vincent, Matthew P. REGISTRATION NUMBER: 36,7
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                                                                                                                                                                            STRANDEDNESS:
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02109
                                                                                                                                                                                            nucleic acid
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b; Pred. No. 1.4
0; Mismatches
                                              Score 52.4; DB 1;
Pred. No. 0.013;
0; Mismatches 196;
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hes 0;
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US-09-050-863-2
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                                                                                                          TELEFAX: (415) 949-8711
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2580 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Silva, ROBIN M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-(
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Rela
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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APPLICANT: Payan, Don
TITLE OF INVENTION: Mammal:
TITLE OF INVENTION: System
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                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE: 30-MA
                                           STRANDEDNESS:
TOPOLOGY: un
                                                                                          TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
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                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                  TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      San Francisco
                                                                                     nucleic acid
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                                              unknown
                                                                                                                                                                                                    (415) 781-1989
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                                                                  unknown
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Query Match Best Local Similarity

2.2%;

Score 46.4; Pred. No. 0

DB 3;

Length 2580;

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US-08-910-647-J
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; ORGANISM: VEBNA
US-09-130-114-1
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                                                                                                                                                                RESULT 10
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                                                                                             Sequence 1, Application US/08910647 Patent No. 6251433 GENERAL INFORMATION:
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Best Local Similarity
Matches 113; Conserva
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APPLICANT: Robbins, Alan K.
TITLE OF INVENTION: Eukaryctic Cells Stably Expressing
TITLE OF INVENTION: From Multiple Transfected Episomes
FILE REFERENCE: 0867/ID903US1
CURRENT APPLICATION NUMBER: US/09/130,114
CURRENT FILING DATE: 1998-08-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 36 SOFTWARE: FastSEQ for Windows Version 3.0
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                                              TITLE OF INVENTION: Compositions and TITLE OF INVENTION: Polynucleotide De
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                                                                                  APPLICANT:
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                    CORRESPONDENCE ADDRESS
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                                   NUMBER OF SEQUENCES:
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 ADDRESSEE:
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                                                                                Zuckermann et al.
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                                                                                                                                                                                                                                                                                Sequence 15, Applicat Patent No. 5316921 GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                                                                            NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech,
COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: patin (Genentech) CURRENT APPLICATION DATA:
                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                           1195 GGAGGGGCAGGAGGAGCAGGAGGGGCAGGAGGGGCAGG
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REFERENCE/DOCKET NUMBER: 12
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 923-2706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Fujita, Sharon M.
                                                                                                                                                                                                                                                 TITLE OF INVENTION:
                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1752 CCACGTGGAGGGCCTGAAGGCGGAGGAGCGGCACCGCCCGGTGCGGGACTGGATCCTACG
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                           STREET: 460 Point San Bruno CITY: South San Francisco
                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: PC-DOS/MS-DOS
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94608-2916
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                                                                                                                          USA
                                                                                                                                                                                                                                               Godowski, Paul J. Lokker, Nathalie A. VENTION: SINGLE-CHAIN HEPATOCYTE GROWTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                              Inc.
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FACTOR VARIANTS
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APPLICATION NUMBER:

US/07/884,811

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                                                                                                                                                                                                                                                                                                                                                                                           Sequence 15, Applicat Patent No. 5328837 GENERAL INFORMATION:
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Best Local Similarity
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-3216
                                                CLASSIFICATION: 530 PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                           COMPUTER READABLE FORM: 85.25 inch, 360 Kb floppy disk
                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS: ADDRESSEE: Genentech,
                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2729 GGAGGGGCAGGAGGGAGCAGGAGGGGCAGGAGGGGCAGG 2772
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                                                                                                                              SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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                ATTORNEY/AGENT INFORMATION:
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                                                                                                                                            OPERATING SYSTEM:
SOFTWARE: patin (
                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 415/77168
THUEX: 910/371-7168
                                                                                                APPLICATION NUMBER: FILING DATE: 199205
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                                                                                                                                                                                                                                                                STATE:
                                                                                                                                                                                                                                                                                 CITY:
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                                   FILING DATE:
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                                                                                                                                                                                                                                                                              South San Francisco
Dreger, Ginger R.
                                                                                                                                                                                                                                                                California
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Pred. No. 0
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Best Local Similarity
Matches 113; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1632 GGAGGATTTGAAGGCGCTCAGTCAGCAGAATGTCAGCATGGACTTGGCCCACGTTCATGAA 1691
REFERENCE/DOCKET NUMBER: POTELECOMMUNICATION INFORMATION:
                                                                                                                                          CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: 07/884811
                                                                                                                                                                                                                                SOFTWARE: WinPatin (Ge
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1692 GCTGCGGACGGATGCGGTGCCGTTGACTGTGGCTGAGGTGCAGAAACTTCTGGGACC 1751
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LENGTH: 10596 bases
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                                                           FILING DATE: 18-MAY-92
ATTORNEY/AGENT INFORMATION:
                                                                                               FILING DATE: 18-MAY-PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 417, 7168
                                                                                                                                                                              APPLICATION NUMBER: US/08/087,783A FILING DATE: 13-Jul-1993 CLASSIFICATION: 435
                             REGISTRATION NUMBER: 35,600
                                                                                                                                                                                                                                                                OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                     COMPUTER:
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TELEFAX: 415/952-9881
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                                                                                                                                                                                                                                                                                                                                                                               STREET: 460 Point San Bru
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                                                     NAME:
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                                               Marschang, Diane L
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SYSTEM: PC-DOS/MS-DOS
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:

910/371-7168

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US-08-194-088B-15; Sequence 15; App
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US-08-194<sub>-</sub>088B-15
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Best Local Similarity 50.4%;
Matches 113; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                  REGISTRATION NUMBER: 32,692
REFERENCE/DOCKET NUMBER: 75:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                            APPLICATION NUMBER: 07/88
FILING DATE: 18-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Gallegos, R. Thomas
REGISTRATION NUMBER: 32,65
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                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 530 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1692 GCTGCGGACGGATGCGGTGCTGCCGTTGACTGTGGCTGAGGTGCAGAAACTTCTGGGACC 1751
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Godowski, Paul J. Lokker, Nathalie A. Mark, Melanie R
TITLE OF INVENTION: SINGLE-CHAIN HEPATOCYTE GROWTH FACTOR VARIANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1812 GCAGCGGCAGGACGACCTGGACACGCTGGGGCTGGGGCTACAGG 1855
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                TELEFAX: 415/--
TELEFAX: 910/371-7168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 10596 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/0 FILING DATE: 09-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                     TELEPHONE:
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                                     STRANDEDNESS:
                                                                          LENGTH:
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                                                                          10596 bases
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1632 GGAGGATTTGAAGGCGCTCAGTCAGCAGAATGTGAGCATGGACTTGGCCACGTTCATGAA 1691

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Best Local
Query Match
Best Local Similarity
Matches 113; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 113; Conserv
                                                                                                                                                                     TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: patin (Genentech) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                        TELEPHONE: 415/225-3216
                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2729 GGAGGGGCAGGAGGAGGAGGAGGGGCAGGAGGGCAGG 2772
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                     TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: 18-MA
                                                                                                                     STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Godowski, Paul J. Lokker, Nathalie A. Mark, Melanie R. VENTION: HEPATOCYTE GROWTH FACTOR PROTEASE DOMAIN VARIANTS
   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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   0; Mismatches 111; Indels
                   Score 46.4; DB 2; Pred. No. 0.33;
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Maximum Match 1008
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Gapop 10.0 , Gapext 1.0
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2138
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.

Score

Query Match Length DB

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Description

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CURRENT APPLICATION NUMBER: US/60/172,360
CURRENT APPLICATION NUMBER: 1999-12-16
NUMBER OF SEQ ID NOS: 29838
SOFTWARE: PERL PROGram
SEQ ID NO 22854
LENGTH: 2126
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME YERV: 1505 foature
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FILE OF INVENTION: Identified Thereby
FILE REFERENCE: GX-0015 P
CURRENT APPLICATION UMBER: US/60/213,359
CURRENT FILING DATE: 2000-06-21
NUMBER OF SEQ ID NOS: 7924
SOFTWARE: PERL Program
SEQ ID NO 6105
LENGTH: 2126
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: 346520.3
US-60-213-359-6105
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US-08-426-819-34
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Ve
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION NUMBER: US/08/426,819
FILLING DATE: 21-APR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MUTPHY JT, GETFALD M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 230-107P
                                                                                                                                                                                                                                                                           TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO:
                                                                                                                      CLONE:
FEATURE:
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LENGTH: 2129 base pairs
TYPE: nucleic acid
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CLONE: pKP027
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HYPOTHETICAL: NO
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                                                                          FEATURE:
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CITY: Falls Church
STATE: Virginia
COUNTRY: USA
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           LOCATION: 1873
OTHER INFORMATION:
OTHER INFORMATION:
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TOPOLOGY: not
                                                        NAME/KEY:
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            /note= 'pKP021"
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2018 GAGCAGGCACGGTGATCCCCGTTCCACCCCAAGAGAAACTCGCGCT	מם סט	ō (B 5
2039 GGAGCAGGCACGGGTGATCCCCGGTTCCACCCCAAGAGAACTCGCGCCT	ОУ	59 TOOGGOOGGTTOOGGGGGAAGTGGAGAAGACACACCCTTOTTOAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA	9
1979 IGECCITARGUECCCACICCCITECIBECCCCAGCCCIGCTGGGGAT	Db	899 CCGCGTGGCGGCAACGCTCCTCTCGGGACCCATCCTGGCGGCGGCAGCCTGAACGGACCCATCC 958	8 8
98	D dy	839 GGGGCCTGCTGCCGGGCCGGGCCAGCCATCATCCGCAGCATCCCGCAGGGCATCGTGG 898	DB 024
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99 AC 78 AC	Qy Db	7	Qy Db
18	Qy Db	659 CTTGCGACCTGCCTGGGCGCTTTGTGGCCGAGTCGGCCGAAGTGCTGCTACCCCGGCTGG 718	Db Qy
1679 CCACGTTCATGAAGCTGCGGACGGATGCGGTGCTGCCGTTGACTGTG	Qy	599 GCTGGGGTGTGCGGGGGTCTCTGCTGAGCGAGGCTCATGTGCGGGGCTCTGGGAGGCCTGG 658	gy Qy
1619 GTGGGGCCCCCACGGAGGATTTGAAGGCGCTCAGTCAGCAGAATGTG	Оу	539 TGGACCTGCTCCCGAGGGGGGCTCCCGAGCGACAGCGGCTGCCTGC	Оy
559 GC 11 538 GC	Qy Db	479 ATGCGTTCTCGGGGCCCCAGGCCTGCACCCGTTTCTTCTCCCGCATCACGAAGGCCAATG 538	Оy
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9 GC	рь	Query Match 93.3%; Score 1994; DB 8; Length 2129; Best Local Similarity 97.0%; Pred. No. 0; Matches 2075; Conservative 0; Mismatches 35; Indels 30; Gaps 3;	¥ & 6

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CAGGCACGGGTGATCCCCCGTTCCACCCCAAGAGAACTCGCGCTCAGTAAAC	Db
GAGCAGGCACGGTGATCCCCGTTCCACCCCAAGAGAACTCGCGCTCAGTAAACGG	УО
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1799 ACTGGATCCTACGGCAGCGGCAGGACGACCTGGACACGTGGGGCTGGGGCTACAGGGCG 18	D Qy
718 AACTTCTGGGACCCCACGTGGAGGGCCTSAAGGCGGAGGGGGACCGCCCGGTGCG	Db
CCCACGTGGAGGGCCTGAAGGCGGAGGAGCGGCACCG	Qy
Db 1658 CCACGTTCATGAAGCTGCGGACGGATGCGGTGCTGCCGTTGACTGTGGCTGCAGA 1717	дb
CACGTTCATGAAGCTGCGGACGGATGCGGTGCTGCCGTTGACTGTGGCTGAGGTGC	Qy
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TGGGGCCCCCACGGAGGATTTGAAGGCGCTCAGTCAGCAGAATGTGAGCATGG	Qy
Db 1538 GCCTTGCTTTCCAGAACATGAACGGGTCCGAATACTTCGTGAAGATCCAGTCCTTCCT	Db
CCTTGCTTTCCAGAACATGAACGGGTCCGAATACTTCGTGAAGATCCAGTCCTTCCT	Qy
1478 GGCCCCAGGACCTGGACACGTGTGACCCCAAGGCAGCTGGACGTCCTCTATCCCAAGGCC	Db
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CCTGGAGGCCTTGAGGCTTTGCTTGAGTCAACAAGGGCACGAATGAGT	Db
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ACCTGGGCTACCTCTTCCTCAAGATGAGCCCTGAGGACATTCGCAAGTG	Db
CACCTGGGCTACCTCTTCCTCAAGATGAGCCCTGAGGACATTCGCAAGT	Qy
Db 1142 TGGACGTCCTAAAGCATAAACTGGATGAGCTCTACCCACAAGGTTACCCCGAGTCTGTGA 1201	Db
GTCCTAAAGCATAAACTGGATGAGCTCTACCCCACAAGGTTACCCCGAGTCTGTG	Qy
Db 1082 CGGCCCTGCCCAGCCCAGATGGCACCGCGTGAACGCCATCCCCTTCACCTACGAGCAGC 1141	Db
CTGCTGGCCACCCAGATGGACCGCGTGAACGCCATCCCCTTCACCTACGAGCAG	Qy
Db 1022 GCGAGATAGACGAGAGCCTCATCTTCTACAAGAAGTGGGAGCTGGAAGCCTGCGTGGATG 1081	Db
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SEQ ID NO 10869
LENGTH: 2433
TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity 97.2%;
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CURRENT FILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 10912
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APPLICANT: Jones, Robert
APPLICANT: Harlocker, Susan L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
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APPLICANT: Pan, Yang

TITLE OF INVENTION: NOVEL NUCLEIC ACID MOL.

TITLE OF INVENTION: THEREFOR

FILE REFERENCE: 1600.1168-001

CURRENT APPLICATION NUMBER: US/09/644,868

CURRENT FILING DATE: 2000-08-28

PRIOR APPLICATION NUMBER: 60/151,063

PRIOR FILING DATE: 1999-08-27

NUMBER OF SEQ ID NOS: 10075

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LENGTH: 2289
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CURRENT APPLICATION THEREFOR
CURRENT APPLICATION UNMBER: US/09/652,12;
CURRENT FILING DATE: 2000-08-30
PRIOR APPLICATION UNMBER: 60/151,134
PRIOR FILING DATE: 199-08-30
NUMBER OF SEQ ID NOS: 10475
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9551
LENGTH: 2289
TYPE: Dan
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Sequence 9551, Application US/0
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Shyjan, Andrew W.
TITLE OF INVENTION: NOVEL NUC
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1600.1183-001
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Sequence 11861, Application US/09698010
GENERAL INFORMATION:
APPLICANT: Williamson, Mark
APPLICANT: Shyjan, Andrew W.
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLE
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1600.2029-001
CURRENT APPLICATION NUMBER: US/09/698,010
CURRENT FILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: 60/162,358
PRIOR FILING DATE: 1999-10-29
NUMBER OF SEQ ID NOS: 15684
SOFTMARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11861
LENGTH: 2289
TYPE: DNA
ORGANISM: Homo Sapiens
US-09-698-010-11861
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RESULT 10
US-09-699-998-8662
; Sequence 8662, App
; GENERAL INFORMATIC
; APPLICANT: Holt; FILE REFERENCE: 1600.2008-001
CURRENT APPLICATION NUMBER: US/09/699,99
CURRENT FILING DATE: 2000-10-30
PRIOR APPLICATION NUMBER: 60/162,362
PRIOR FILING DATE: 1999-10-29
NUMBER OF SEQ ID NOS: 10905
SOFTWARE: FastSEQ for Windows Version 4
SEQ ID NO 8662
LENGTH: 2289
TYPE: DNA APPLICANT: Holtzman,
APPLICANT: Gearing, D
TITLE OF INVENTION: N
TITLE OF INVENTION: T Sequence 8662, Application: ORGANISM: Homo Holtzman, Application sapiens NOVEL NUCLEIC THEREFOR 36666960/sn Þ ACID MOLECULES

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2037 1925 2097 1985

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; SOFTWARE: FastSEQ for W:

; SEQ ID NO 2725

; LENGTH: 2289

; TYPE: DNA

; ORGANISM: Homo sapiens

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Matches 2053; Conserv
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CURRENT APPLICATION NUMBER: US/09/710,280
CURRENT FILING DATE: 2000-11-10
PRIOR APPLICATION NUMBER: 60/164,537
PRIOR FILING DATE: 1999-11-10
NUMBER OF SEQ ID NOS: 2763
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APPLICANT: Gearing, David P.
TITLE OF INVENTION: MOVEL NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREFOR
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TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1600.2036-001
CURRENT APPLICATION NUMBER: US/09/710,28
CURRENT FILING DATE: 2000-11-10
PRIOR APPLICATION NUMBER: 80/164,254
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 5803
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SOFTWARE: Fast
SEQ ID NO 4128
FENGTH: 2289
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Best Loc
Matches
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GENERAL INFORMATION:
APPLICANT: Hunter, John J.
APPLICANT: Shylan, Andrew W.
APPLICANT: Stbdal, Hilde
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-09-710-281-4128
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APPLICANT: Gearing, David P.
APPLICANT: McCarchy, Sean A.
APPLICANT: HOLTZMAN, Douglas A.
APPLICANT: HOLTZMAN, Douglas A.
TITLE OF INVENTION: NOVEL NUCLEIC ACID PRIOR ETERENCE: 1600.2005-001
CURRENT APPLICATION NUMBER: US/09/710,280
CURRENT FILING DATE: 2000-11-10
PRIOR APPLICATION NUMBER: 60/164,255
PRIOR APPLICATION NUMBER: 60/164,255
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4115
SOFTWARE: FastSEQ for Windows Version 4
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; TYPE: DNA
; ORGANISM: HOMO :
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GENERAL INFORMATION:
APPLICANT: Gearing, David P.
APPLICANT: Holtzman, Douglas A.
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SOFTWARE: FastSEQ for Windows
SEQ ID NO 1716
LENGTH: 2289
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Best Local Similarity
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CURRENT FILING DATE: 2000-11-29
PRIOR APPLICATION NUMBER: 60/167,845
PRIOR FILING DATE: 1999-11-29
NUMBER OF SEQ ID NOS: 2579
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GENERAL INFORMATION:
APPLICANT: Ma, Xiao-Jun
TITLE OF INVENTION: Tumor Associated Molecules (TAMS):
FILE REFERENCE: 3214
CURRENT APPLICATION NUMBER: US/60/164,285
CURRENT FILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 8259
SEQ ID NO 821
LENGTH: 1108
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Best Local Similarity
Matches 1086; Conserv
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                        AAGTGGGAGCTGGAAGCCTGCGT-GGATGCGGCCCTGCTGGCCACCCAGATGGACCGCGT
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                                                                                 gaacgccatccccttcacctacgagcagctggacgtcctaaagcataaactggatgagct
                                                                                                              GAACGCCATCCCCTTCACCTACGAGCAGCTGGACGTCCTAAAGCATAAACTGGATGAGCT
                                                                                                                                       aagtgggagctggaaccatgcgtaggatgcggccctgctggccacccagatggaccgcgt
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96.3%;
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Pred. No. 3.6e-155;
0; Mismatches 14;
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CCCAAGAGAACTCGCGCTCAGTAAACGGGAACATGCCCCCTGCAGACA 2115
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                                                                                                                                                                                                                                                                                                                      AGGCGGAGGAGCGCCCCGCCCGGTGCGGGACTGGATCCTACGGCAGCGGCAGGACGACC 1828
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                                                                                            CCCAGCCCTGCTGGGGATCCCCGCCTGGCCAGGAGCAGGCACGGGTGATCCCCGTTCCAC 2067
                                                                                                                                      CCGTCCTGGCACTGCTAGCCTCCACCCTG-GCCTGAGGGCCCCACTCCCTTGCTGGC 2007
                                                                                                                                                                                                                                                            TGGACACGCTGGGGCTACAGGGCGGCATCCCCAACGGCTACCTGGTCCTAGACC 1888
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                                                                                                                                                                                 tcagcatgcaacatggcctctcggggacgccctgcctcctaggacctggacctgttctca
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Search completed: December 7, 2001, 10:40:45 Job time: 2818 sec

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Result
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/1/pna/P

2: /cgn2_6/ptodata/1/pna/U

3: /cgn2_6/ptodata/1/pna/U

4: /cgn2_6/ptodata/1/pna/U

5: /cgn2_6/ptodata/1/pna/U

5: /cgn2_6/ptodata/1/pna/U
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Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Copyright (c) 1993 - 2000 Comp
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442

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US-09-815-264-79254

US-09-249-585A-2

US-09-724-876-2

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US-60-325-448-4349

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US-09-815-264-766673
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67667, Appli
58041, A
2426, Ap
76667, A
76667, A
76667, A
79054, A
80054, A
8044, Appli
4340, Ap
4340, Ap
82984, A
86091, A
86091, A
86356, A
86356, A
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126, App
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US-09-388-906A-23028	US-09-799-462A-17	US-09-815-264-82641	US-09-815-264-82390	US-09-815-264-73824	US-09-760-446A-523	US-09-815-264-65084	US-09-815-264-62575	US-09-815-264-82752	JS-09-388-906A-20855	US-09-388-906A-10829	US-09-388-906A-17125	US-09-815-264-62252	US-09-815-264-77573	JS-09-815-264-64392	US-09-815-264-67258	PCT-US01-27760-93	US-09-822-846A-23
Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
23028, A	17, Appl	82641, A	82390, A	73824, A	523, App	65084, A	62575, A	82752, A	20855, A	10829, A	17125, A	62252, A	77573, A	64392, A	67258, A	`	23, Appl

ALIGNMENTS

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US-09-828-792-48

Sequence 48, Application US/09828792

GENERAL INFORMATION:
APPLICANT: Gearing, David P.
APPLICANT: Robison, Keith E.
APPLICANT: Holtzman, Douglas A.
APPLICANT: Holtzman, Douglas A.
TITLE OF INVENTION: Nucleic Acid Molecules Derived from a
TITLE OF INVENTION: Human Fetal Lung Library
FILE REFERENCE: MLM98-34Pa
CURRENT APPLICATION NUMBER: US/09/828,792
CURRENT FILING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: US/09/330,360
PRIOR APPLICATION NUMBER: 05/09/330,360
PRIOR APPLICATION NUMBER: 05/09/330,360
PRIOR APPLICATION NUMBER: 05/090,258
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 05/090,258
PRIOR FILING DATE: 1998-06-22
NUMBER OF SEO ID NOS: 1102
                                                                                                                                                                                                                                                                                                                                                                                                ; NAME/KEY: CDS
; LOCATION: (133)...(562)
; NAME/KEY: misc_feature
; LOCATION: (1)...(562)
; OTHER INFORMATION: n = A,
US-09-828-792-48
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SEQ ID NO 48
LENGTH: 562
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
                     185 TGCATCCCGCGAGGACCCTGGCTGGAGAGACAGGGACGGAGTCTGCCCCCCTGGGGGGAG
224 tgcagccctcgaggaccctggctggagagacagggcaggaggctgcacccctggacggag
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les 487; Conservative
                                                                                                                                                                       TGCCTCCCTCGGGATCTACACAGACCATGGCCTTG - CAACGGCTCGACCCCTGTTGG
                                                                            ggtcctgtgggacccccgccctcggcagcctcctgttcctgctcttcagcctcggatggg
                                                                                                TCCTGTGGGGACCGCCC-----TGGCAGCCTCCTGTTCCTGCTCTTCAGCCTCGGATGGG
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: LOCATION: (31)...(553)
: NAME/KEY: misc_feature
: LOCATION: (1)...(553)
: OTHER INFORMATION: n = A,T,C
US-09-828-792-182
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PRIOR APPLICATION NUMBER: 60/090,258
PRIOR FILING DATE: 1998-06-22
NUMBER OF SEQ ID NOS: 1102
SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 182
LENGTH: 553
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Best Local
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CURRENT FILING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: US/09/330,360
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APPLICANT: Robison, Keith E.
APPLICANT: Holtzman, Douglas A.
TITLE OF INVENTION: Nucleic Acid Molecules Derived
TITLE OF INVENTION: Human Fetal Lung Library
FILE REFERENCE: MLN98-34Pa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 553
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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                ATTTCCAGCCTCTCCCCCCCCAACTCCTTGGCTTCCCGTGTGCGGAGGTGTCCGGCCTG
                                                                                      GCTGGAGAGACAGGGAGTCTGCCCCCCTGGGGGGAGTCCTGACAACCCCCCATAAC
                                                                                                                                                        --TGGCAGCCTCCTGTTCCTGCTCTTCAGCCTCGGATGGGTGCATCCCGCGAGGACCCTG 204
atttccagcctctcccctcgccaactccttggcttcccgtgtgcggaggtgtccggcctg
                                                                      gctggagagacagggcaggaggctgcacccctggacggagtcctggccaacccaacctaac
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C
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Pred. No. 2.2e-82;
0; Mismatches 26
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FEATURE:

NAME/KEY: CDS
LOCATION: (78)...(442)
NAME/KEY: misc_feature
LOCATION: (1)...(442)
OTHER INFORMATION: n = A
US-09-828-792-151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US/99/330,360
PRIOR FILING DATE: 1999-06-11
PRIOR APPLICATION NUMBER: 60/990,258
PRIOR FILING DATE: 1998-06-22
NUMBER OF SEQ ID NOS: 1102
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 151
LENGTH: 442
TYPE: DNA
ORGANISM: Homo sapiens
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GENERAL INFORMATION:
APPLICANT: Gearing, David P.
APPLICANT: Robison, Keith E.
APPLICANT: Holtzman, Douglas A.
TITLE OF INVENTION: Nucleic Acid Molecules Derived
TITLE OF INVENTION: Human Fetal Lung Library
FILE REPERENCE: MLN98-34Pa
CURRENT APPLICATION NUMBER: US/09/828,792
CURRENT FILING DATE: 2001-04-09
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Best Local
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ATTTCCAGCCTCTCCCCTCGCCAACTCCTTGGCTTCCCGTGTGCGGAGGTGTCCGGCCTG
                                gctggagagacagggcaggaggctgcacccctggacggagtcctggccaacccacctaac
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                                                                                                                     Conservative
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92.4%;
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                                                                                                                                                                                                                                                                                                                Score 357.8; DB 5;
Pred. No. 6.3e-68;
0; Mismatches 27;
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                                                                                                                                                                                                                                                                                                                                               Length
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US-60-325-795-1
; Sequence 1, Application US/60325795
; GENERAL INFORMATION: .
; APPLICANT: Su, Eric W
; APPLICANT: Wang, He
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TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.484C6
CURRENT APPLICATION NUMBER: US/09/970,966
CURRENT FILING DATE: 2001-10-02
NUMBER OF SEQ ID NOS: 215
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 126
LENGTH: 396
TYPE: DNA
ORGANISM: Homo sapiens
US-09-970-966-126
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Best Local Similarity 80.9%;
Matches 279; Conservative
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APPLICANT: Fling, Steven P.
APPLICANT: Xu, Jiangchun
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Pred. No. 3.5e-38;
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; LOCATION: (18)..(2306)
; OTHER INFORMATION:
US-60-325-795-1
; LOCATION: (1)..(4282)
; OTHER INFORMATION: n = a,c,g,t any unknown
US-09-778-927A-16
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                                                                                                                                                                                                                                                                                                                                                          Sequence 16, Application US/09778927A
GENERAL INFORMATION:
APPLICANT: KHOSRAVI, Rami et al.
TITLE OF INVENTION: NOVEL NUCLEIC ACID AND AMINO ACID
TITLE OF INVENTION: VARIANTS OF ALTERNATIVE SPLICING
FILE REFERENCE: 2786-0160P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/60/325,795
CURRENT FILING DATE: 201-09-28
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
LENGTH: 2511
TYPE: DNA
                                                                                                                                             SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 16
.LENGTH: 4282
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Best Local Similarity
Matches 157; Conserv
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                                                                                                                                                                                                            PRIOR FILING DATE: 2000-03-29
NUMBER OF SEQ ID NOS: 81
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TITLE OF INVENTION: NOVEL SECRETED PROTEINS AND THEIR USES
                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER:
                                                         FEATURE: misc_feature
                                                                                                   ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
                                                                                                                              TYPE: DNA
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US-09-815-264-67667
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Best Local Similarity 47.5%;
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SEQ ID NO 67667
LENGTH: 19363
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Best Local Similarity 49.5%;
Matches 161; Conservative
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Genomic Plant Sequences And FILE REFERENCE: 38-21(51237)G CURRENT APPLICATION NUMBER: US/09/815,264 CURRENT FILING DATE: 2001-03-23
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              17829 gccgacgtgcacgtcgctggtggcgcagcggtggacgcgccgctcgccgccgtgtggcc
                                                                                              17769 cgtggtgcgcgcaccacacgttcccggcggcggagcgcgcgggggggcggggggg
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                                                                                                                                           1728 TGAGGTGCAGAAACTTCTGGGACCCCACGTGGAGGGCCCTGAAGGCGGAGGAGCGGCACCG
                                                                                                                                                                                                      1668 CATGGACTTGGCCACGTTCATGAAGCTGCGGACGGACGGGTGCCGTTGCCGTTGACTGTGGC 1727
                                                           1788 CCCGGTGCGGACTGGATCCTACGGCAGCGGCAGGACCTGGACACGCTGGGGGCTGGG 1847
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                                                                                                                                                                                                                                                                                        Score 52; DB 5; Length 19363; Pred. No. 0.23;
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: Sequence 58041, Application US/09815264

: GENERAL INFORMATION:
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US-09-815-264-58041
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PRIOR FILING DATE: 2000-10-31
NUMBER OF SEQ ID NOS: 109669
SEQ ID NO 58041
LENGTH: 17466
TYPE: DNA
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Best Local Similarity
Matches 141; Conserv
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CURRENT FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: US 09/620,392
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TITLE OF INVENTION: Genomic Plant Sequences
FILE REFERENCE: 38-21(51237)G
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11485 CTCGAGGAGACGTTCTCGAGCTCCAGCCTGCTGCAGATGATCTCCATGTCGCC 11433
                                                                                                                                                                               11605 GAGCTCGCCGTCGCCTGCCTGAGCGCCCGAGAACGGGCTCTGCATGCTCGGCGTCGCC 11546
                                                                                                                                                                                                                                                                     11665 GTGACGCTCCTGGCGGGGAAGCAGCTGCCGGCGCCGAACGAGGACGTGAGGAAGGTGTTC 11606
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                                                                                        1627 CCCACGGAGGATTTGAAGGCCTCAGTCAGCAGAATGTGAGCATGGACTTGGCCCACGTTC 1686
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                                       1867 AACGGCTACCTGGTCCTAGACCTCAGCGTGCAAGAGACCCTCTCGGGGACGCC 1919
                                                                                                                                1807 CTACGGCAGCGGCAGGACGACCTGGACACGCTGGGGCTACAGGGCGGCATCCCC 1866
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                                                                                                                                                                                                                                                                                                               1687 ATGAAGCTGCGGACGGATGCGGTGCTGCCGTTGACTGTGGCTGAGGTGCAGAAACTTCTG 1746
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Koshi, Jeffrey M.
Kovalic, David K.
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NN NUMBER: 60/236,327 FE: 2000-09-29 NN NUMBER: 60/241,785 PE: 2000-10-20 NN NUMBER: 60/244,617 NN NUMBER: 60/244,617 NN NUMBER: 60/25,268 FE: 2000-08-14 NN NUMBER: 60/236,368 PE: 2000-09-29 NN NUMBER: 60/251,856 NN NUMBER: 60/251,856 NN NUMBER: 60/251,856 NN NUMBER: 60/251,856 NN NUMBER: 60/251,868 PE: 2000-12-08	N NUMBER: 60/235, 834 TE: 2000-09-27 N NUMBER: 60/234, 274 N NUMBER: 60/234, 223 N NUMBER: 60/234, 223 N NUMBER: 60/228, 924 N NUMBER: 60/224, 518 N NUMBER: 60/224, 518 N NUMBER: 60/236, 369 TE: 2000-08-14 N NUMBER: 60/236, 369 TE: 2000-09-29 N NUMBER: 60/236, 369 N NUMBER: 60/236, 369 TE: 2000-09-29 N NUMBER: 60/236, 369 TE: 2000-07-26 N NUMBER: 60/241, 809 TE: 2000-11-17	NUMBER: 6 1 2000-08 1 WIMBER: 6 2000-08 1 WIMBER: 6 2000-07 NUMBER: 6 2000-07 NUMBER: 6 2000-08 NUMBER: 6 2000-08 1 2000-08 1 2000-08 1 2000-08	ce 2456, Application US/09760446A L INFORMATION: CANT: Rosen et al. OF INVENTION: Nucleic Acids, Proteins, OF INVENTION: Nucleic Acids, Proteins, INT APPLICATION NUMBER: US/09/760,446A NT ETLING DATE: 2000-01-16 APPLICATION NUMBER: 60/179,065 FILING DATE: 2000-02-04 APPLICATION NUMBER: 60/218,628 FILING DATE: 2000-02-04 APPLICATION NUMBER: 60/217,487 APPLICATION NUMBER: 60/217,487 FILING DATE: 2000-06-28 APPLICATION NUMBER: 60/217,487 FILING DATE: 2000-08-14 APPLICATION NUMBER: 60/225,758 FILING DATE: 2000-08-14 APPLICATION NUMBER: 60/227,963 APPLICATION NUMBER: 60/227,963 APPLICATION NUMBER: 60/227,496 FILING DATE: 2000-07-11 APPLICATION NUMBER: 60/227,496
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Best Local
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APPLICATION NUMBER: 60/
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APPLICATION NUMBER: 60/249,214
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APPLICATION NUMBER: 60/249,297
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APPLICATION NUMBER: 60/249,215
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                                                                                                                                                                               GCTTGCGACCTGCCTGGGCGCTTTGTGGCCGACTCGGCCGAAGTGCTGCTACCCCGGCTG 717
                                                                                                                                                                                                                     tgtaggggtgtgtgaaggggtgttcagcacaaaggggctgcaggctctctgggaagcgtg 9596
                                                                                                                                                                                                                                                                                                           97; Conserv
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                                                                                                                                                                                                                                                                                                       Score 49; DB 5; Length 11720; Pred. No. 0.84; 0; Mismatches 80; Indels
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US-09-815-264-72273
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LENGTH: 17403
TYPE: DNA
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 09/620,392
PRIOR FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: US 09/702,134
PRIOR FILING DATE: 2000-10-31
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CURRENT FILING DATE: 2001-03-23
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8741 CGCGGACGAGGCAGAGGCGGCGG 8719
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                                                                                                                                                                                                                                                                                                                                      707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 587 CGGCTCTGGCCTGCGGGGTGTGCGGGGGGTCTCTGCTGAGCGAGGCTGATGTGCGGGGTC 646
                                    947 AACGGACCATCCTCCGGCCGCGG 969
                                                                                                              AGGGCATCGTGGCCGCGTGGCGGCAACGCTCCTCTCGGGACCCATCCTGGCGGCAGCCTG 946
                                                                                                                                                                                                                            AGGCGAGGCGGCGGCTGGATCTGAGTGGAGTGGCGGCGGTGCTAGCGGAGGTGGCGGTCA
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                                                                         GTGGACGCGCGGAGGTGGTCGCGGGCAAGCGGCGCCCTCATGGAGGCGGCGGCGGT 8742
                                                                                                                                                  CGGATGAGCGGCGCACTCGTGGAGGCGGCGGCGGCGGCGGCGGCGGCGCGCTC
                                                                                                                                                                                   TGGACGCTCTGCGGGGCCTGCCTGCCCGCCCATCATCCGCAGCATCCCGC 886
                                                                                                                                                                                                                                                                                                                           TCACGGTGCTCGTGGAGGTGGCGGCAGTCATGGACCAAGCGGAGGAGGCGCCGGGCGCGCG
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McIninch, James
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ic, David K.
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45.4%;
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Pred. No. 1.2;
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US-09-815-264-76667; Sequence 76667, Application US/09815264; GENERAL INFORMATION:

APPLICANT: Boukharov, Andrey A.

TITLE

OF INVENTION: Genomic Plant Sequences And Uses Thereof

APPLICANT:

APPLICANT:

PPLICANT:

APPLICANT: APPLICANT:

ROVALIC, David K. Dotson, Stantor Koshi, Jeffrey Cao, Yongwei

Stanton B.

Liu, Jingdong McIninch, James

APPLICANT: APPLICANT:

FILE REFERENCE: 38-21(51237)G

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APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
TITLE OF INVENTION: Genomic Plant Sequences And
FILE REFERENCE: 38-21(51237)G
CURRENT APPLICATION UNMBER: US/09/815,264
CURRENT FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: US 09/620,392
PRIOR FILING DATE: 2000-07-19
PRIOR FILING DATE: 2000-07-19
PRIOR FILING DATE: 2000-10-31
NUMBER OF SEQ ID NOS: 109669
SEQ ID NO 76673
LENGTH: 76304
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                                                                                                                                             ; NAME/KEY: unsure
; LOCATION: (1)..(76304)
; OTHER INFORMATION: unsure at all n locations
US-09-815-264-76673
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US-09-815-264-76667
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Best Local Similarity
Matches 115; Conserv
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SEQ ID NO 76667
LENGTH: 50229
TYPE: DNA
                                            Matches
                                                             Query Match
Best Local Similarity
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CURRENT FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: US 09/620,392
PRIOR FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: US 09/702,134
PRIOR FILING DATE: 2000-10-31
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                                                                                                                                                                                                                               FEATURE:
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1756 GTGGAGGGCCTGAAGGCGGAGGAGCGCCACCGCCCGGTGCGGGACTGGATCCTACGGCAG 1815
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1756 GTGGAGGGCCTGAAGGCGGAGGAGCGGCACCGCCCGGTGCGGGACTGGATCCTACGGCAG 1815
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Kovalic, David K.
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                                            Conservative
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Pred. No. 2.6;
0; Mismatches 112;
                                                             Score 47.8;
Pred. No. 3;
                                          .Mismatches 112;
                                                                               DB 5;
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: LOCATION: (1)..(9648)
: OTHER INFORMATION: unsure at all n locations
US-09-815-264-80624
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PRIOR FILING DATE: 2000-10-31
NUMBER OF SEQ ID NOS: 109669
SEQ ID NO 80624
LENGTH: 9648
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Best Local Similarity 43.5%;
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Sequence 80624, Application US/09815264
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TITLE OF INVENTION: Genomic Plant Sequences
FILE REFERENCE: 38-21(51237)G
CURRENT APPLICATION NUMBER: US/09/815,264
CURRENT FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: US 09/620,392
PRIOR FILING DATE: 2000-07-19
PRIOR FILING DATE: 2000-07-19
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5776 tggacgaggcgacgagcgcgctggacgtgyagtcggagcgcgtcgtgcagcaggcgctgg 5835
                                                1250 AGTGGAATGTGACGTCCCTGGAGACCCTGAAGGCTTTGCTTGAAGTCGACAAAGGGCACG 1309
                                                                                            5716 nnnnnnnnnnnnnnnnnnnnncgcgcgcgccatcgtgaaggacccggccatcctgctcc 5775
                                                                                                                                          1190 AGTCTGTGATCCAGCACCTGGGCTACCTCTTCCTCAAGATGAGCCCTGAGGACATTCGCA 1249
                                                                                                                                                                                         5656 gcgcgctgccggagggctaccggacgagagtcggggagcgcgggggtgcagcnnnnnnnnn 5715
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                                                                                                                                                                                                                                                                                                           1070 GCGTGGATGCGGCCCTGCTGGCCACCCAGATGGACCGCGTGAACGCCATCCCCTTCACCT 1129
                                                                                                                                                                                                                                                                                                                                                                          5536 agcaagagccggcgctgttcgcgacgaccatctacgacaacatcctctacgggaaagacg 5595
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Kovalic, David K.
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Pred. No. 1.
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US-09-815-264-79254/c

5836 a 5836

Sequence 79254, Application US/09815264

ENERAL INFORMATION:

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NAME/KEY: unsure
LOCATION: (1)..(49792)
OTHER INFORMATION: unsure at all n locations
US-09-815-264-79254
                                                                                                                                                                                                                                                                           US-09-249-585A-2
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                                                                                                                                 Sequence 2, Application US/09249585A
GENERAL INFORMATION:
APPLICANT: Horlick, Robert
TITLE OF INVENTION: METHOD FOR MAINTENANCE AND SELECTION OF
FILE REFERENCE: 0867/D905
CURRENT APPLICATION NUMBER: US/09/249,585A
CURRENT FILING DATE: 1999-02-11
                                  NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin version 3.0
SEQ ID NO 2
LENGTH: 1926
TYPE: DNA
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Best Local Similarity
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PRIOR FILING DATE: 2000-10-31
NUMBER OF SEQ ID NOS: 109669
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PRIOR APPLICATION NUMBER: US 09/620,392
PRIOR FILING DATE: 2000-07-19
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CURRENT APPLICATION NUMBER: US/09/815,264
CURRENT FILING DATE: 2001-03-23
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TITLE OF INVENTION: Genomic Plant Sequences
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TYPE: DNA
ORGANISM: Oryza sativa
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                  ORGANISM: Epstein Barr Virus
FEATURE:
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Kovalic, David K.
Liu, Jingdong
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; LOCATION: (1)..(1926)
; COTHER IMPORMATION: coding strand of EBNA-1 DNA
US-09-249-585A-2
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Best Local Similarity 50.4%;
Matches 113; Conservative
                                                                               1812 GCAGCGGCAGGACGACCTGGACACGCCTGGGGCTGCGGCCTACAGG 1855
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ALIGNMENTS

	source	FEATURES			COMMENT	JOURNAL	TITLE	AUTHORS	REFERENCE		ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	LOCUS	RESULT 1 AL574127/c
/db_xref="taxon:9606" /db_xref="taxon:9606" /clone="050D1040YH04" /clone="1b="LTI_NELO06_PL2" /tlssue_type="placenta" /note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pcMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Lilang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371	/organism="Homo sapiens"	Location/Qualifiers	Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.	Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France	Contact: Genoscope	Unpublished (2001)	Full-length cDNA libraries and normalization	Li,W.B., Gruber,C., Jessee,J. and Polayes,D.	1 (bases 1 to 1037)	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Homo sapiens	human.	EST.	AL574127.1 GI:12934032	ALS74127	AL574127 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0DI040YH04 3		

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                                         TGAAGGGAAGGGCCAGCTAGACAAAGACACCCTAGACACCCTGACCGCCTTCTACCCTG
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                     AGGGCGGCATCCCCAACGGCTACCTGGTCCTAGACCTCAGCGTGCAAGAGACCCTCTCGG
                                                                                        TGCAGAAACTTCTGGGACCCCACGTGGAGGGCCCTGAAGGCGGAGGAGCGGCACCGCCCGG
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Pred. No. 1.4e-135;
2; Mismatches 3;
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Contact: Genoscope
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/note="Vector: pcMVSpORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pcMVSpORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact: Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax: (1) 301 610 8371
Email: filang@lifetech.com URL:
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923 bp LTI_NFL006_PL2 RNA sequence.

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1 (bases 1 to 923)
Li,W.B., Gruber C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
Bp 191 91006 EVRY cedex - France
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//note="vector: pcmySpORT 6; Site_1: NotI; 1st strand cDNA
//note="vector: pcmySpORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pcMySpORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact: Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockwille, Maryland 20850, USA Fax: (1) 301 610 8371
Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com"
57 a 276 c 301 g 176 t 3 others
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Location/Qualifiers
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prime, mRNA sequence.
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Full-length cDNA libraries
Unpublished (2001)
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1. (bases 1 to 933)
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/note="Vector: pcWVSpORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
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a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax: (1) 301 610 8371
Email: filang@lifetech.com URL:
http://fulllength.invitrogen.com"

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/db_xref="taxon:9606"
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Pred. No. 4.5e-118;
3; Mismatches 16;
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Full-length cDNA libraries
Unpublished (2001)
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BP 191 91006 EVRY cedex - France
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1 (bases 1 to 968)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: seqref@genoscope.cns.fr,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CSOD1086Y101"
/clone="LTI_NFL006_PL2"
/clone_tib="LTI_NFL006_PL2"
/tissue_type="placenta"
/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand
was primed with a NotI-oligo(dT) primer. Five prime
was primed with a NotI-oligo(dT) primer.
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Pred. No. 1.4e-117;
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Genoscope - Centre Nationa
BP 191 91006 EVRY cedex -
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length CDNA libraries and normalization
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/clone="CSODKNO2YCO6"
/clone_lib="LTI_NFL006_PL2"
/tissue_type="placenta"
/tissue_type="placenta"
/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact: Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax: (1) 301 610 8371
Email: fliang@lifetech.com URL:
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/db_xref="taxon:9606"
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                                                                     TTCCAGCCTCTCCCCCTCGCCAACTCCTTGGCTTCCCGGTGTGCGGAGGTGTCCGGCCTGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                              a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email: filang@lifetech.com URL: http://fulllength.invitrogen.com" 340 c 314 g 171 t 5 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="placenta"
/note="Vector: pcMvSpORT 6; Site_1: NotI; 1st strand cDNA
/note="Vector: pcMvSpORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pcMvSpORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact: Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
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                                                                                                                Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
                                                                                                                                             Contact: Genoscope
                                                                                                                                                           Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
                                                                                                                                                                                                                                                                                  EST
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AL514070 LTI_NFL006_PL2
                                                                                                                                                                                                     Mammalia; Eutheria;
1 (bases 1 to 912)
                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                Homo sapiens
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                                                                                                                                                                                                                                                                 human.
                                                                                                    segref@genoscope.cns.fr,
                           /db_xref="taxon:9606"
/clone="CL0BA004ZG08"
/clone_lib="LTI_NFL006_PL2"
/tissue_type="placenta"
                                                         /organism="Homo sapiens'
                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                        Homo sapiens cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Vector: pcMvSPORT 6; Site_1: NotI; 1st strand cDNA was primed with a NotI oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the NotI and Eco RV sites of the pcMvSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email: flang@lifetech.com URL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://fulllength.invitrogen.com"
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4; Mismatches 39;
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Email: cgapbs-remail.nlh.gov

This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the This clone is a state of the This contact                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AI056902 726 bp mRNA EST 29-SEP-19 oz03h07.x1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens clone; IMAGE:1674301 3' similar to TR:014859 Q14859 PRE-PRO-MEGAKARYOCYTE POTENTIATING FACTOR PRECURSOR. ;, mRN
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Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 436.
Location/Qualifiers
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National Cancer Institute, Cancer Genome Anat
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1 (bases 1 to 726)
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/lab_host="DH10B (amplicillin resistant)"
/note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
This is a subtracted version of the original Soares fetal
liver spleen 1NFLS library. 1st strand cDNA was primed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            liver spleen 1NFLS library. 1st strand cDNA was with a Pac I - oligo(dT) primer (5'
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/db_xref="taxon:9606"
/clone="IMAGE:1674301"
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Pred. No. 5.7e-99;
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Contact: Genoscope
                                                                                             Genoscope - Centre National de
BP 191 91006 EVRY cedex - Franc
Email: segref@genoscope.cns.fr,
Location/Qualifiers
                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 817)
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           /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CSODKOO2yCO6"
/clone_ib="LTI_NFL006_PL2"
/tissue_type="placenta"
/note="Vector: pCMVSPORT 6; 5
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2 LTI_NFL006_PL2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Life Technologies catalog #: 11548-013
DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 2146 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
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/db_xref="taxon:9606"
/clone="IMAGE:2421584"
/clone="ib="NCI_CGAP_Pan1"
/tissue_type="adenocarcinoma"
/lab_host="DH10B"
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Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.72 kb. Life Technologies catalog #:
11548-013"
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                                                                                                                                                                                                             High quality sequence stop: 419.
Location/Qualifiers
                                                                                                                                                                                                                                                found through the I.M.A.G.E. Consortium/LLNL www.bio.llnl.gov/bbrp/image/image.html Insert Length: 1518 Std Error: 0.00 Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                       Life Technologies catalog #: 11548-013
DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                               Tumor Gene Index Unpublished (1997)
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                    11548-013"
                                   /note="Organ: pancreas; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.72 kb. Life Technologies catalog #:
                                                                                       /tissue_type="adenocarcinoma"
/lab_host="DH10B"
                                                                                                                          /clone="IMAGE:2511112"
/clone_lib="NCI_CGAP_Pan1"
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Mammalia; Eutheria; F
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NCI-CGAP http://www.n
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CDNA Library Preparation: Life Technologies, Inc
CDNA Library Arrayed by: Greg Lennon, Ph.D.
CDNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    quality sequence stop: 403
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note-"Organ: ovary; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: Not1; Cloned unidirectionally, Primer: Oligo dT. Average insert size 1.35 kb. Tumor types include: mixed Mullerian tumor, papillary serous, clear cell, spindle cell. All are primary tumors, metastasis positive. Life Technologies catalog #: 11534-013"

244 c 266 g 150 t 6 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="NCI_CGAP_Ov23"
/tissue_type="tumor, 5 poo
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2218269"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /SIDS2/qcqdata
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3261
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/SIDS2/gcgdata/geneseq/geneseqp/AA1981.DAT:*
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/SIDS2/gcgdata/geneseq/geneseqp/AA1000.DAT:*
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AAW26674
AAB753992
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AAR53991
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AAR53980
AAR53991
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                                                                                                                                      Human CAK1 antigen
Megakaryoctye pote
Mesothelin related
Soluble mesothelin
                                                                                                                                                                                                                                      Description
                                                       Meg-Pot fragment.
Meg-Pot N-terminal
Meg-Pot fragment.
                    Protein sequence
                                          Human
                                                                                                                    Mesothelin related
glutamicum
                                        leucine-rich
prote
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T. thermophilus DN	AAR13143	12	834	3.1	101.5	45
Mutant thermostabl	AAR23164	13	789			44
Mutant thermostabl	AAR23165	13	758		101.5	43
213	AAB42371	21	1084		102.5	42
Human protein sequ	AAB93780	22	790	3. <u>1</u>	102.5	41
Human protein sequ	AAB95160	22	546		102.5	40
Human CLASP-3 prot	AAB99495	22	2090		. 103	39
Mutant thermostabl	AAR26476	13	834		103	38
Bovine DNA-depende	AAY17386	20	941		103.5	37
DNA polymerase I h	AAR96203	17	834		103.5	36
	AAR99542	17	834		103.5	ω 5
Human peripheral b	AAY53970	21	1857		104	34
	AAW59945	19	836		104.5	ω ω
 Amino acid sequenc 	AAW59944	19	836	٠	104.5	32
Protein encoded by	AAW59943	19	834		104.5	31
	AAR79149	16	834		104.5	30
Heat stable DNA po	AAR43998	15	834		104.5	29
Glutamic acid rece	AAR45945	15	1239		105	28
Fission yeast prot	AAW13387	18	804		105.5	27
Murine APLP1. Mus	AAR98903	17	653		106.5	26
	AAG07306	21	337		107	25
eryA region polype	AAR44431	14	3567	٠	107.5	24
	AAW61369	19	1288	•	107.5	23
Non-reducing sacch	AAY85166	21	757	•	107.5	22
б	AAY85151	21	756		107.5	21
	AAG38206	21	340	3.4	110.5	20
Arabidopsis thalia	AAG07304	21	349		111	19
	AAG07305	21	346		111	18
Phospholipase A2 (AAB74535	22	913		113.5	17
Human phospholipas	AAB82415	22	913	•	113.5	16
n PLA2	AAY51557	21	913	•	113.5	15
Meg-Pot fragment.	AAR53989	15	23		114	14
thali	382	21	351	3. 5	114.5	13
Arabidopsis thalia	AAG38205	21	349		114.5	12

ALIGNMENTS

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AAW26674
                                                                                                                                                                                                                                                                                                          RESULT
                                                                                                                                      Cleavage-site
                                                                                                                                                                                                     CAK1 antigen; mesothelin; tumour specific antigen; mesothelioma; ovarian cancer; squamous cell cancer; therapy; vaccine; diagnosis
                                                                                                                                                                                                                                Human CAK1 antigen (mesothelin).
                                                                                                                                                                                                                                                    11-MAR-1998
                                                                                                                                                                                                                                                                      AAW26674;
                                                                                                                                                                                                                                                                                       AAW26674 standard; Protein; 628
                          05-JAN-1996;
                                                             17-JUL-1997.
                                                                                                                    Region
                                                                                                                                                                                   Homo sapiens
                                           03-JAN-1997;
                                                                                WO9725068-A2.
                                                                                                                                                                   Key
      (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                         Peptide
                                                                                                                                                                                                                                                   (first entry)
                          96US-0010166.
                                           97WO-US00224
                                                                                                                                    /note= "putative membrane insertion signal" 292..293
                                                                                                                      /note= "putative furin processing site"
587..628
                                                                                                                                                        Location/Qualifiers 16..32
                                                                                                            /note=
                                                                                                 "hydrophobic tail typical for GPI anchorage"
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          bearing an antigen comprising at least 10 contiguous amino acids of mesothelin involves: (a) providing a chimeric molecule comprising the effector molecule attached to a targeting molecule that specifically binds to mesothelin; and (b) contacting the tumour with the chimeric molecule such that the chimeric molecule specifically binds to a tumour cell. Also claimed is a method for inhibiting mesothelin expression or activity by contacting mesothelin bearing cells with inhibitory nucleic acids for the mesothelin gene. The methods can be used to detect tumour cells and to inhibit the growth of cells bearing mesothelin. Mesothelin derived antigens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mesothelin. Its amino acid sequence was deduced from a cDNA clone (see AAT91079) isolated from a HeLa cDNA library. A 40 kDa form (K1) of mesothelin that is found on the surface of human ovarian tumour OVCAR-3 cells appears to be derived from the 69 kDa precursor by several processing steps. A claimed method for specifically delivering an effector molecule to a tumour cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   on mesorhelium, mesorhelionas, ovarian cancers and some squamous cell carcinomas. The antigen has been designated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mesotheliomas or ovarian tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             growth of cells bearing mesothelin. Mesothelin-derived antmay be used in vaccines for the inhibition or prevention of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This protein comprises the human CAK1 antigen which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 58-60; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Agents for targeting mesothelin, a tumour cell antigen - used for
the detection or inhibition of growth of e.g. mesotheliomas, ovarian
cancers and squamous cell carcinomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chang K,
481
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                                                                                                 LLFLNPDAFSGPQACTRFFSRITKANVDLLPRGAPERQRLLPAALACWGVRGSLLSEADV
                                  IDRFVKGRGQLDKDTLDTLTAFYPGYLCSLSPEELSSVPPSSIWAVRPQDLDTCDPRQLD
                                                                                                                                                               PSGKKAREIDESLIFYKKWELEACVDAALLAT@MDRVNAIPFTYE@LDVLKHKLDELYP@
                                                                                                                                                                                                                              stmdalrgllpvlgqpiirsipqgivaawrqrssrdpswrqpertilrprfrrevektac
                                                                                                                                                                                                                                                                STMDALRGLLPVLGQPIIRSIPQGIVAAWRQRSSRDPSWRQPERTILRPRFRREVEKTAC
                                                                                                                                                                                                                                                                                             ralgglacdlpgrfvaesaevllprlvscpgpldqdqqeaaraalqgggppygppstwsv
                                                                                                                                                                                                                                                                                                               RALGGLACDLPGREVAESAEVLLPRLVSCPGPLDQDQQEAARAALQGGGPPYGPPSTWSV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 3261; DB 18; Length 628; 100.0%; Pred. No. 2.3e-289;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                   Query Match
Best Local Similarity
Matches 601; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-OCT-1992;
11-NOV-1992;
09-DEC-1992;
                                                                                                                                                                                                                                                                                                                   DNA encoding the 584 or 248 amino acid prod. use in treatment of thrombocytopenia and low
                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 52-57; 74pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1994-167467/20.
N-PSDB; AAQ63972.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hattori K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                              New mega:karyoctye potentiator -
thrombocytopenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CHUS ) CHUGAI SEIYAKU KK.
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                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kojima
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92JP-0286153.
92JP-0301387.
92JP-0329546.
                                                                                                                                                                                                                                                                            AA;
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39..286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers 39..622
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-:
                                                                                                                                                                 Score 3053; DB 15;
Pred. No. 2.4e-270;
3; Mismatches 16;
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                                                                                                                                                                                                              Length
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                                                                                                                                                                   Gaps
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Diagnosing carcinomas, e.g. adenocarcinoma or ovarian carcinomas, detecting reactivity of a molecule (with an antigenic determinant present in a sample) with an antibody specific for a mesothelin reantigen polypeptide
                                                                                                                                                                                                           Mesothelin; mesothelin related antigen; MRA; malignant condition; cancer; differentiation antigen; adenocarcinoma; mesothelioma; ovarian carcinoma; pancreatic carcinoma; non-small cell lung carcinoma; MRA-2.
                                                                                                          26-FEB-1999;
05-AUG-1999;
                                                                                                                                                                                                                                                 Mesothelin
                                                                                                                                                                                                                                                                                                     AAB08544 standard;
                                                                        Scholler NB,
                                                                                                                                      25-FEB-2000; 2000WO-US04834.
                                                                                                                                                         31-AUG-2000
                                                                                                                                                                         WO200050900-A2
                                                                                                                                                                                                                                                                  20-DEC-2000
                                                                                                                                                                                                                                                                                   AAB08544;
                                                                                        (PACI-) PACIFIC NORTHWEST RES FOUND
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DB; AAA64363.
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                                                                       Hellstrom
                                                                                                          99US-0121767.
99US-0147404.
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                                                                                                                                                                                                                                                (MRA)-2
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                                                                       Hellstrom
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Best Local S
Matches 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     591 GYLVLDLSVO
|||||||||||
| 293 gylvldlsvq
                        Scholler
                                                                                                                   26-FEB-1999;
05-AUG-1999;
                                                                                                                                                                                        25-FEB-2000; 2000WO-US04834
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                                                                                                                                                                                                                                                                                                                                                                                  pancreatic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-DEC-2000
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                                                                    (PACI-) PACIFIC NORTHWEST RES FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                471
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                        Hellstrom
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99US-0147404
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97.18;
                        Ι,
                                                                                                                                                                                                                                                                                                                                                                           elated antigen; MRA; malignant
  adenocarcinoma; mesothelioma;
n-small cell lung carcinoma; MR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SMR) antigen polypeptide sequence
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Pred. No. 5.5e
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                        Hellstrom
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5.5e-133;
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ovarian car
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Best Local Similarity
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25-FEB-2000; 2000WO-US04834.
                                                                                                                                                                                                                                              differentiation antigen; adenocarcinoma; mesothelioma; ovarian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Diagnosing carcinomas, e.g. adenocarcinoma or ovarian carcinomas, by detecting reactivity of a molecule (with an antigenic determinant and present in a sample) with an antibody specific for a mesothelin related antigen polypeptide
                                                        31-AUG-2000.
                                                                                                                                                                                                                       pancreatic carcinoma; non-small cell lung carcinoma; MRA-1.
                                                                                                                                                                                                                                                                          Mesothelin; mesothelin related antigen; MRA; malignant condition;
                                                                                                                                                                                                                                                                                                                                Mesothelin related antigen (MRA)-1 polypeptide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB08543 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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Pred. No. 7.5e-133;
1; Mismatches 0;
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Best Local
                                               Megakaryoctye potentiator; Meg-Pot; thrombocytopenia; platelet; amplification; primer; polymerase chain rea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents a human mesothelin related antigen (MRA)-1. Antibodies specific to MRA polypeptides are used for the detection of a malignant condition. Mesothelin is a differentiation antigen which is expressed in the surfaces of normal mesothelial cells and also on certain cancer cells, including epithelial ovarian tumours and mesotheliomas. The method is useful for detecting the presence of a malignant condition, specifically, adenocarcinoma, mesothelioma, ovarian carcinoma, pancreatic carcinoma or non-small cell lung carcinoma
                                                                                                                                 Meg-Pot fragment
                                                                                                                                                                                         08-DEC-1994
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05-AUG-1999;
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reactivity of a molecule (with an antigenic determinant and
in a sample) with an antibody specific for a mesothelin related
polypeptide .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                 standard; peptide; 65
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99US-0147404.
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97.18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1531; DB 21;
Pred. No. 2.2e-131;
1; Mismatches 0;
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                                                     reaction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 399;
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                                                     PCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8
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Best Local Similarity
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        23-OCT-1992;
11-NOV-1992;
09-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-OCT-1992;
11-NOV-1992;
09-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Use of the primers given in AAQ77809-10 in PCR resulted fragments given in AAQ63971.
DNA encoding Meg-Pot has potential use in treatment of
                                            25-OCT-1993;
                                                              11-MAY-1994.
                                                                               WO9410312-A
                                                                                                         Key
Misc-difference
                                                                                                                                     Homo sapiens
                                                                                                                                                        platelet.
                                                                                                                                                               Megakaryoctye potentiator; Meg-Pot; thrombocytopenia;
                                                                                                                                                                                  Meg-Pot N-terminal peptide
                                                                                                                                                                                                    08-DEC-1994
                                                                                                                                                                                                                       AAR53988
                                                                                                                                                                                                                                        AAR53988 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                       \ensuremath{\mathsf{UNA}} encoding Meg-Pot has potential use in treatment of thrombocytopenia and low platelet function.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 51; 74pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New mega:karyoctye potentiator -
thrombocytopenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1994-167467/20.
N-PSDB; AAQ63971.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hattori K, Kojima T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CHUS ) CHUGAI SEIYAKU KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-OCT-1993;
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                                                                                                                                                                                                                                                                                     lnpda 65
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                                                                                                                                                                                                                                                                                                                                                                                                          65 AA;
                                                                                                                                                                                                                                                                                                                                                            10.0%; Score 325; DB 15; llarity 100.0%; Pred. No. 2.8e-22; Conservative 0; Mismatches 0;
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92JP-0301387.
92JP-0329546.
       92JP-0286153.
92JP-0301387.
92JP-0329546.
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                                             93WO-JP01540
                                                                                                           Location/Qualifiers
                                                                                                  /note= "residue not identified"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oh-eda
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Best Local Similarity 97.1%;
Matches 34; Conservative
                                                                                                                                                                                                                        23-OCT-1992;
11-NOV-1992;
09-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR53990;
Sequence
                    Use of the primers given in AAO77805-08 in PCR resulted fragments given in AAO63969-70. The properties given in AAO63969-70 in treatment of DNA encoding Meg-Pot has potential use in treatment of thrombocytopenia and low platelet function.
                                                                                                    New mega: karyoctye potentiator \cdot for potential treatment of thrombocytopenia
                                                                                                                                        WPI; 1994-167467/20.
N-PSDB; AAQ63970.
                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                  Megakaryoctye potentiator; Meg-Pot; thrombocytopenia; platelet; amplification; PCR
                                                                                                                                                                                                                                                                                                                                                                                                    Meg-Pot fragment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA encoding Meg-Pot
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                                                                               Disclosure; Page 50; 74pp; Japanese
                                                                                                                                                                            Hattori K,
                                                                                                                                                                                                                                                                       25-OCT-1993;
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25 AA;
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                                                                                                                                                                          Kojima T,
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92JP-0301387.
92JP-0329546.
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                   has potential use in treatment low platelet function.
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Pred. No. 7.1e-08;
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Query Match Best Local Similarity

3.9%;

Score 128; DB 15; Pred. No. 6.7e-05;

Length 25;

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RESULT
AAE03600
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                                                                                                                                                                                                                                                                                                                                                                                                                                           amyotrophic lateral sclerosis; epilepsy; psychiatric disorder; mania; depression; schizophrenia; anxiety; phobic disorder; learning disorder; memory disorder; amnesia; migratine; protein protein interaction; cellular activity; neoplastic transformation; drug screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human leucine-rich repeat-containing protein, AZAD.
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Alzheimer's disea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; leucine-rich repeat;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     identification; gene therapy.
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s disease; dementia; Parkinson's disease; multiple sclerosis;
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192..215
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                                                                                                                                                                                                                                                                                                                                                                      /label= Signal_peptide 59..794
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                note= "Leucine-rich
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                                   "Leucine-rich
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disorders e.g. amnesia of age-related memory loss, and neurological disorders e.g. migraine. AZAD molecules are useful as markers of disorders or disease states, as markers for precursors of disease state, for predisposition of disease state or as markers of drug activity or pharmacogenomic profile of a subject. The AZAD polypeptide and polynucleotide are capable of modulating protein-protein interaction, e.g. by interacting with an extracellular component, thereby modulating cellular activities, including attachment, adhesion, migration, patterning, growth and/or differentiation of a cell. AZAD proteins are and function, pathological conditions, e.g. neuronal degeneration, neoplastic transformation and tumour progression. AZAD proteins are neoplastic transformation and tumour progression. AZAD proteins are
                                                                                                                                                        useful as immunogens to raise anti-AZAD antibodies which are useful to detect and isolate AZAD proteins and modulate its activity. AZAD proteins are useful to screen for naturally occurring AZAD substrates and to screen for drugs or compounds which modulate AZAD activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           epilepsy, psychiatric disorders e.g. depression, schizophrenic disorders, mania, anxiety or phobic disorders, learning or memory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New leucine-rich repeat-containing protein and nucleic acid molecules for diagnosing, treating neural disorders, such as neurodegenerative disorders, such as Alzheimer's disease, dementia, epilepsy and prostate
                                                                                                                      AZAD nucleic acid fragments are useful as primers or hybridisation probes for the detection of AZAD-encoding nucleic acids. cDNA encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Parkinson's disease, multiple sclerosis, amyotrophic lateral sclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and cancer (e.g. adenocarcinoma, prostate cancer, genitourinary system carcinomas and testicular tumour). The neurodegenerative disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and a prostate disorder, e.g. prostatitis, benign prostatic hyperplasia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diagnosing AZAD-mediated or related disorders, which includes a neural disorder (e.g. neurodegenerative disorders, including CNS disorders)
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N-PSDB; AAD08044.
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                                                                                                 the AZAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is name. Secreted protein, AZAD. AZAD polypeptide is useful for secreted protein, AZAD. AZAD polypeptide its activity and binds to identifying a compound which modulates its activity and binds to identifying a compound which modulates are useful for treating.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AZAD proteins and nucleic acid molecules are useful
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                                          AD protein are useful in gene therapy. AZAD sequences are also to map their respective genes on a chromosome, for tissue type forensic identification of a biological sample.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mour). The neurodegenerative disorders
dementias related to Alzheimer's disease.
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Query Match

Sequence

794

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Best Local Similarity

3.8%;

Score Pred.

123.5; DB No. 0.037;

22;

Length 794;

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RESULT 10
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                                                                                                            The present invention relates to human JAFFA polyhuclevilves (New AAF90326) and polyheptides (see AAB82351). JAFFA is a novel membe of the fibroblast growth factor family. JAFFA proteins may be useful for developing novel diagnostic and therapeutic agents for JAFFA-associated disorders such as cancers and ABO(H) blood group disorders, and for controlling cellular proliferative and/or disorders, and for controlling cellular proliferative and/or
                        used to treat and/or diagnose a variety of immune disorders such as autoimmune disease and multiple sclerosis. JAFFA nucleic acids may also be used to express JAFFA protein, to detect JAFFA mRNA or a genetic alteration in a JAFFA gene, and to modulate JAFFA activity. Note: The present sequence is given in the Sequence Listing from
                                                                                                                                                                                                                                                                                 Isolated JAFFA nucleic acid molecules which encode novel fibroblast growth factor family members (JAFFA) are useful for developing novel diagnostic and therapeutic agents for JAFFA-associated disorders suc
                                                                                          disorders, and for controlling certural process and proteins may be differentiative disorders. JAFFA nucleic acids and proteins may be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB82352 standard; Protein;
                                                                                                                                                                                                                                   Disclosure; Page 129-131; 137pp; English.
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within the specification
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              invention, but does not
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07-APR-2000;
03-AUG-2000;
                                                                                                                                                                                Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                                                                                                                                                                                  Nakagawa
Tateishi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Coryneform bacterium; ar organic acid synthesis.
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DB; AAH66664.
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; 2000JP-0280988.
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Senoh A, Ikeda
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Ozaki A;
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The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum are useful for identifying the mutation point of a gene derived from the corynery of the

of coryneform bacterium,

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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                               AAG38205;
                                                       AAG38205 standard; Protein; 349 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GSLLSEADVRALGGLACDLPGREVAESAEVLLPRLVSCPGPLDQDQQEAARAALQGGGPP 231
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07-MAY-1999;
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17-JUN-1999;
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Matches 92; Conservative
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222 klaenlenddfrkatttl--prfqqe-----
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Pred No. 0.06
53; Mismatches
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0.069;
nes 128;
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23-JUL-1999 99US-0145 23-JUL-1999 99US-0145 23-JUL-1999 99US-0145 26-JUL-1999 99US-0145 27-JUL-1999 99US-0145 27-JUL-1999 99US-0145 27-JUL-1999 99US-0145 27-JUL-1999 99US-0146 02-AUG-1999 99US-0146 02-AUG-1999 99US-0146 02-AUG-1999 99US-0146 02-AUG-1999 99US-0146 02-AUG-1999 99US-0147 04-AUG-1999 99US-0147 04-AUG-1999 99US-0147 05-AUG-1999 99US-0147 09-AUG-1999 99US-0147 09-AUG-1999 99US-0147 09-AUG-1999 99US-0147 09-AUG-1999 99US-0147 09-AUG-1999 99US-0147 09-AUG-1999 99US-0147	20000000000000000000000000000000000000	29-JUN 1999; 99US-014 30-JUN 1999; 99US-014 01-JUL-1999; 99US-014 02-JUL-1999; 99US-014 06-JUL-1999; 99US-014 06-JUL-1999; 99US-014 08-JUL-1999; 99US-014 09-JUL-1999; 99US-014 12-JUL-1999; 99US-014 13-JUL-1999; 99US-014 14-JUL-1999; 99US-014 14-JUL-1999; 99US-014	18-JUN-1999; 99US-013 22-JUN-1999; 99US-013 23-JUN-1999; 99US-014 24-JUN-1999; 99US-014 24-JUN-1999; 99US-014 24-JUN-1999; 99US-014	N-1999; 99US-0133 N-1999; 99US-0133

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3.5%;
20.7%;
Score 114.5; DB 21;
Pred. No. 0.07;
        Length 351;
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RESULT 14
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11-NOV-1992;
09-DEC-1992;
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                            Disclosure; Page 50; 74pp; Japanese
                                                                                                      WPI; 1994-167467/20.
N-PSDB; AAQ63969.
                                                                                                                                                                                                                                                                                                                                                                                             Megakaryoctye potentiator; Meg-Pot; thrombocytopenia;
platelet; amplification; primer; polymerase chain reaction;
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Use of the primers given in AAQ77805-08 in
                                                          New mega:karyoctye potentiator thrombocytopenia
                                                                                                                                                Hattori K, Kojima T,
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92JP-0329546.
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                                                                                          This invention describes a novel human phospholipase A2 (PLA2) protein (I) and its encoding nucleic acid. The amino acid (I) releases arachidonic acid in specific tissues characterized by unique membrane phospholipids, by generating lysophospholipid species which are deleterious to membrane integrity or by remodeling of unsaturated species of membrane phospholipids through deacylation/reacylation mechanisms. The amino acid is useful in assays to identify inhibitors having a therapeutic benefit, such as inhibiting the central role of PLA2 in the inflammatory component of Alzheimer's disease. The amino acid (I) allows sensitive and rapid screening and identification of inhibitors of phospholipase A2. This sequence represents the human PLA2 protein (also known as phosphatide 2-acyl hydrolase).
                                                                                                                                                                                                                                                                       Claim 1; Column 53-58; 32pp; English.
                                                                                                                                                                                                                                                                                                     An isolated amino acid having phospholipase (PL)A2 activity is useful in assays to identify inhibitors having a therapeutic benefit, such as inhibiting the central role of PLA2 in the inflammatory component of Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PLA2; phospholipase A2; phosphatide 2-acyl hydrolase; human; therapy; arachidonic acid; lysophospholipid; Alzheimer's disease.
                                                                     Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fragments given in AAQ63969-70.
DNA encoding Meg-Pot has potent
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                                                                                                                           nlyaanlqdslywasepsqfwdrwvrnqanldkeqvpllkieeppstagriaefftdllt
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phlclldvgyli-----ntscl
                                -----GYLVLDLSVQETLSGTPCL 609
                                                             wrplagathnflrglhfh--kdyfqhphfstw----kattld-----glpngltpse
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Search completed: December 7, 2001, 10:01:37 Job time: 720 sec

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd

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Maximum
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ALIGNMENTS

RESULT 1 US-08-776-271-2

Sequence 2, Application Patent No. 6083502 GENERAL INFORMATION:

US/08776271

; MOLECULE TYPE: protein US-08-776-271-2	C *:
-5	٠.
; TYPE: amino acid	٠.
; LENGTH: 628 amino acids	٠.
; SEQUENCE CHARACTERISTICS:	٠.
; INFORMATION FOR SEQ ID NO: 2:	٠.
; TELEFAX: (415) 576-0300	٠.
; TELEPHONE: (415) 576-0200	٠.
; TELECOMMUNICATION INFORMATION:	٠.
; REFERENCE/DOCKET NUMBER: 015280-259100US	٠.
; REGISTRATION NUMBER: 41,739	٠.
; NAME: Faris, Susan K.	٠.
; FILING DATE: 05-JAN-1996	٠.
; APPLICATION NUMBER: US 60/010,166	٠.
; PRIOR APPLICATION DATA:	٠.
; FILING DATE: 03-JAN-1997	٠.
; APPLICATION NUMBER: WO PCT/US97/00224	٠.
PRIOR APPLICATION DATA:	٠.
; CLASSIFICATION: 424	٠.
; FILING DATE: 01-DEC-1998	٠.
; APPLICATION NUMBER: US/08/776,271	٠.
; CURRENT APPLICATION DATA:	٠.
; SOFTWARE: PatentIn Release #1.0, Version #1.30	٠.
OPERATING SYSTEM: PC-DOS/MS-DOS	
; COMPUTER: IBM PC compatible	٠.
; MEDIUM TYPE: Floppy disk	٠.
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; CITY: San Francisco	٠.
STREET: Two Embarcadero Center, Eighth Floor	
; ADDRESSEE: Townsend and Townsend and Crew LLP	
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INVENTION:	
INVENTION: Present on	
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GENERAL INCOMMITTON:	

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Score 3261;

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Length 628;

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ADDRESSEE: Townsend and T
STREET: Two Embarcadero C
CITY: San Francisco
STATE: California
۸,
                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                              APPLICANT: Pastan, Ira
APPLICANT: Chang, Kai
TITLE OF INVENTION: Mesothel
TITLE OF INVENTION: present
TITLE OF INVENTION: and Meth
                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
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                          APPLICATION
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No. 6153430
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Present on Mesothelium, Mesotheliomas and Ovarian Cancers
and Methods and Kits for Targeting the Antigen
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Best Local Similarity
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REFERENCE/DOCKET NUMBER: 01:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 61
FILING DATE: 05-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Faris, Susan K.
REGISTRATION NUMBER: 41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 628 amino acids
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                                                                 TVAEVQKLLGPHVEGLKAEERHRPVRDWILRQRQDDLDTLGLGLQGGIPNGYLVLDLSVQ
                                                                                                                                         VLYPKARLAFQNMNGSEYFVKIQSFLGGAPTEDLKALSQQNVSMDLATFMKLRTDAVLPL
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                                      ETLSGTPCLLGPGPVLTVLALLLASTLA
                                                                                                                             VLYPKARLAFQNMNGSEYFVKIQSFLGGAPTEDLKALSQQNVSMDLATFMKLRTDAVLPL
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03-JAN-1997
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Pred. No. 1.5e-303;
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Best Local Similarity
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GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 230-107P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/426,819A
FILING DATE: 21-APR-1995
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                                                   SVSTMDALRGLLPVLGQPIIRSIPQGIVAAWRQRSSRDPSWRQPERTILRPRFRREVEKT 298
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                     ACPSGKKAREIDESLIFYKKWELEACVDAALLATQMDRVNAIPFTYEQLDVLKHKLDELY
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22040-0747
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T: P.O. Box 747
Falls Church
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Oh-Eda, Masayoshi
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Pred. No. 7.8e-284;
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                                                                                                                                 TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: MUTPHY JT., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 230-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
CORRESPE: Birch, Stewart, Kolasch & Birch
STREET: P.O. Box 747
CITY: Falls Church
STATE: Virginia
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APPLICATION NUMBER: US/0
FILING DATE: 21-APR-1995
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Kojima, Tetsuo
APPLICANT: Oh-Eda, Masayoshi
HYPOTHETICAL: FRAGMENT TYPE:
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                                      MOLECULE TYPE:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
                                                      STRANDEDNESS: not relevant TOPOLOGY: not relevant
                                                                                            TYPE: amino acid
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                                                                                                              LENGTH:
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                                                                                                                584 amino acids
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Query Match
Best Local Similarity
Matches 576; Conserv

Conservative

2

Score 2956; DB 1; Pred. No. 2.1e-274; 2; Mismatches 6;

Length 584; Indels

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Gaps

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US-08-426-819A-37
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                                                                                                                                  ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
APPLICANT:
                                               SOFTWARE: PatentIn Release #1.0, V.
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/425,819A
FILING DATE: 21-APR-1995
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch
STREET: P.O. Box 747
CITY: Falls Church
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                  APPLICANT: Oh-Eda, Masayoshi
APPLICANT: Hattori, Kunihiro
TITLE OF INVENTION: Genes Coc
TITLE OF INVENTION: Potentiat
ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald
REGISTRATION NUMBER: 28,
                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                       USA
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Oh-Eda, Masayoshi
                                                                                                                                                                                                                                                                                                                                                                                                                            Yamaguchi, No.
, Gerald M.
ER: 28,977
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Best Local Similarity 97.6
Matches 242; Conservative
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INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 248 amino acids
                                                                                                                                                                                                                                                                                                                 APPLICANT: Yamaguchi, No. 5723:
APPLICANT: KOjima, Tetsuo
APPLICANT: Kojima, Tetsuo
APPLICANT: Hattori, Kunihiro
TITLE OF INVENTION: Genes Codii
TITLE OF INVENTION: Potentiato:
NUMBER OF SEQUENCES: 37
                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL
                                                                                                                                                                   COUNTRY: UŠA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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TELECOMMUNICATION INFORMATION:
              ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald M.
REGISTRATION NUMBER: 28,977
                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 21-APR-19
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HYPOTHETICAL: FRAGMENT TYPE:
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                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                    ADDRESSEE: Birch, Stewart, Kolasch & Birch
STREET: P.O. Box 747
CITY: Falls Church
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
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STRANDEDNESS: no
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TELEFAX: 703-205-8050
REFERENCE/DOCKET NUMBER:
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97.6%;
                                                                                                                                                                                                                                                                                                                     Potentiator 37
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                                                                                            US/08/426,819A
              28,977
                                                                                                                                                                                                                                                                                                                                                                                                                   5723318omi
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; Pred. No. 2.
1; Mismatche
230-107P
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TELECOMMUNICATION INFORMATION:

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Best Local Similarity 100
Matches 65; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             atent No.
                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 703-20 INFORMATION FOR SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: MULPHY JT., Gerald M.
REGISTRATION NUMBER: 28 977
REFERENCE/DOCKET NUMBER: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
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                                                                                                                                   MOLECULE TYPE: PHYPOTHETICAL: NO FRAGMENT TYPE: 1
                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: 703-205-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: P.O. Box 747
CITY: Falls Church
STATE: Virdinia
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                                                                                                MMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: 21-APPLICATION: 435
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NAME/KEY:
                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: no
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TOPOLOGY: linear
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5723318
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Oh-Eda, Masayoshi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hattori, Kunihiro
                                                                                                                                                                                                                                       not relevant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      230-107P
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Best Local Similarity 100.0%; Pred. No. 2.5e-13;
O: Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No. 572331
                             TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/426,81
FILING DATE: 21-APR-1995
                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: 703-205-8000
                                                                                                                                   ATTORNEY/AGENT INFORMATION: NAME: Murphy Jr., Gerald
                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Oh-Eda, Masayosni
APPLICANT: Hattori, Kunihiro
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LOCATION:
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OTHER INFORMATION: /label= fragment
OTHER INFORMATION: /note= "sequence of cyanogen bromide fragment representing
OTHER INFORMATION: C-terminus of MegPOT determined in Example 28"
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                                                                                                                 NAME: Murphy Jr., Gerald M. REGISTRATION NUMBER: 28,977
                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                            STATE:
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                                                                                                                                                                                                                                                                                                                                                         Virginia
                                                                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oh-Eda, Masayoshi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= fragment /note= "sequence of cyanogen bromide fragment of MegPOT cDNA in Table 3" \,
                                                                                                                                                                                                                                     Release #1.0, Version #1.30
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SEQ ID NO 2
LENGTH: 6095
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Best Local Similarity 23.6
Matches 143; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/144,085
CURRENT FILING DATE: 1998-08-31
EARLIER APPLICATION NUMBER: 09/010,809
EARLIER FILING DATE: 1998-01-22
NUMBER OF SEQ ID NOS: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Betlach, Mary C.
APPLICANT: Ashley, Gary
APPLICANT: Julien, Bryan
APPLICANT: Ziermann, Rainer
TITLE OF INVENTION: SORANGIUM POLYKETIDE SYNTHASES
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 30062-20020.20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Gustafsson,
                                                                                                                                                                                                2975
                                                 3083 QLEQELAAKVKGAWHLHQLLGKRELDAFVLYGSIAGLWGSGAQA----GYGAANAGLDAL 3138
                                                                                                                       3030 RGIRVTLAACDVS----ERA-QLAALLAE--LEQDEAPLRAVAHLAGIGRRVPLRELEPE 3082
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                                                                                        112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: Peptide LOCATION: 6..33 OTHER INFORMATION: OTHER INFORMATION:
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                151 PRGAPERQRLLPAALACWG---
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TOPOLOGY: not
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                                                                                    DLD-----ALPLDLLLFLNP-DAF----
                                                                                                                                                          ----LGFPCAEVSGLSTERVRELAVALAQKNVKLSTEQLRCLAH------RLSE-PPE 111
                                                                                                                                                                                             GWKPRGTVLITGGVGGLGGHLARWLAGR-GAEHL----VLASRRGASAPGASELRDELVA 3029
                                                                                                                                                                                                                                GDRPGSLLFLLFSLGWV--HPARTLAGETGTESAPLGGVLTTPHNISSLSPRQL-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claes
                                                                                                                                                                                                                                                                                   4.1%; Score 134; DB 4; Length 6095; 23.6%; Pred. No. 0.019;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5.0%; Score 163; DB 1; 97.1%; Pred. No. 6.4e-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= peptide
/note= "region of Glu-C peptide having low
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label-
/note- "
                                                                                                                                                                                                                                                                   64; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                -VRGSLLSEADVRALGGLACDLP-G 192
                                                                                      --SGPQACTRFFSRITKANVDLL 150
                                                                                                                                                                                                                                                                   217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AND ENCODING
                                                                                                                                                                                                                                                                   Indels 182;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/09460145 Patent No. 6287838 GENERAL INFORMATION:
                                                                                                                          TELEFAX: (617)
INFORMATION FOR SEQ
                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3493 DAYALT 3498
                                                                                 SEQUENCE CHARACTERISTICS: LENGTH: 778 amino acids
                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Kriz, Ron
APPLICANT: Song, Chuanzheng
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MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                     TOPOLOGY:
                                     STRANDEDNESS
                                                                                                                                                                    TELEPHONE:
                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Cambridge
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                                                           amino acid
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87 CambridgePark Drive
                                                                                                                                            (617)
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                   linear
                                                                                                                                                                    (617) 498-8224
                                                                                                                    7) 422
) 876-5851
~ NO: 2:
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                                                                                                                                                                                                                                                                                                                    08/788,975
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                                                                                                                                                                                                                                                                                                                          RESULT
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                                                                                                                                                                                                                                     Sequence 4, Application US/09460145
Patent No. 6287838
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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                                                                                                                                                 APPLICANT: Kriz, Ron
APPLICANT: Song, Chuanzheng
TITLE OF INVENTION: CYTOSOLIC PHOSPHOLIPASE A2-BETA ENZYMES
NUMBER OF SEQUENCES: 9
                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute,
STREET: 87 CambridgePark Drive
  COMPUTER READABLE FORM:
                                                 STREET: 87 Cambridge CITY: Cambridge STATE: MA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                164 HRVQLVV--PGSCEGPQEASVGTGTFRFHCPACWEQELSIRLQDAPEEQLKAPLSALPSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 560 WRPLAQATHNFLRGLHFH--KDYFQHPHFSTW----KATTLD-----GLPNQLTPSE 605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        265 IVAAWRQRS-SRDPSWRQPERTILRPRFRREVEKTACPSGKKAREIDESLIFYKKWELEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   222 QVVRLVFPTSQEPLMRVELKKEAGLRELAVRLGFGPCAEEQAFLSRRKQVVAAALRQALQ
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                      COUNTRY: UZIP: 02140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MELKVFDQDLVTGDDP--VLSVLFDAGTLR-----AGEFRRESFSLSPQGEGRLEVEFRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SGSTWALANLYEDPEWSQKD-------LAGPT-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NLYAANLQDSLYWASEPSQFWDRWVRNQANLDKEQVPLLKIEEPPSTAGRIAEFFTDLLT 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEYFVKIQSFL--GGAPTE--DLKALSQQNVSMDLATFMKLR------TDAVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LTTFEFGEWCEFSPYEVGF---PKYGAFIPSELFGSEFFMGQLMKRLPESRICFLEGIWS
                                       USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3.5%; Survey 20.8%; Pred. No. user 72; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 113.5; DB Pred. No. 0.059;
                                                                                                                      Inc
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Best Local Similarity
Matches 143; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 797 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: BLOWN, SCOTT A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: GI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: protein
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  539
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                                                                                                                                                            439 LTAFYPGYLCSLSPEELSSVPPSSIWAVRFQDLDTCD--PRQLDVLYPKARLAF-QNMNG
                                                                                                                                                                                                 416 --NLWALINEALLHDEPHDHKLSDQREALSHGQNPLPIYCAL----NTKGQ-----S
                                                                                                                                                                                                                                       384 KWNVTSLETLKALLEVDKGHEMSPQAP-----RRPLPQVATLIDRFVKGRGQLDKDTLDT 438
                                                                                                                                                                                                                                                                                                                                                                  351 SGSTWALANLYEDPEWSQKD-------LAGPT------------
                                                                                                                                                                                                                                                                                                                                                                                                                                               301 LDGDLQEDEIPVVAIMATGGG------IRAMTSLYGQLAGLKELGLLDCVSYITGA 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              209 CPGPLDQDQQEAARAALQGGGPPYGPPSTWSVSTMDALRGLLPVLGQ----PIIRSIPQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 QVVRLVFPTSQEPLMRVELKKEAGLRELAVRLGFGPCAEEQAFLSRRKQVVAAALRQALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           183 HRVQLVV--PGSCEGPQEASVGTGTFRFHCPACWEQELSIRLQDAPEEQLKAPLSALPSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                117 PLDLLLFLNPDAFSGPQACT-----RFF-SRITKANVDLLPRGAPERQRLLPAALACWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57 SSLSPRQLLGFPCAEVSGLSTERVRELAVALAQKNVKLSTEQLRCLAHRLSEPPEDLDAL 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92 MELKVFDQDLVTGDDP--VLSVLFDAGTLR----AGEFRRESFSLSPQGEGRLEVEFRL
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  --PLTVAEVQKLLGPHVEGLKAEERHRPVRDWILRQRQDDLDTLGLGLQGGIPN-----
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                                       NLYAANLQDSLYWASEPSQFWDRWVRNQANLDKEQVPLLKIEEPPSTAGRIAEFFTDLLT
                                                                             SEYFVKIQSFL--GGAPTE--DLKALSQQNVSMDLATFMKLR--
                                                                                                                                                                                                                                                                                                                                                                                                     IVAAWRORS-SRDPSWRQPERTILRPRFRREVEKTACPSGKKAREIDESLIFYKKWELEA 323
                                                                                                                    LTTFEFGEWCEFSPYEVGF---PKYGAFIPSELFGSEFFMGQLMKRLPESRICFLEGIWS
                                                                                                                                                                                                                                                                                  ----ELLKTQVTKNKLGVLAPSQLQRYRQELAERARLGYPSCFT---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----VRGSLLSEADVR----ALGGLACDLPGREVAESAEVL---LPRLVS
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Gaps

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US-08-827-208-3
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 60/04
FILING DATE: 19-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Gaylo, Paul J.
REGISTRATION NUMBER: 36,808
                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: (317) 276-0756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/014,608
ETLING DATE: 29-MAR-1996
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: HUMAN PHOSPHOLIPASE A2
TITLE OF INVENTION: NUCLEIC ACID COMPOUNDS
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                                    117 PLDLLLFLNPDAFSGPQACT-----
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                                                                         261 QSLADR------GEWLVS----NGVLVARELSCLHVQLEETGDQKSSE
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                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                             Local Similarity 20.8 es 143; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
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                                                                                                                                                                                      1 MALQRLDPCWSCGDRPGSLLFLLFSLGWVHPARTLAGETGTES---APLG-GVLTTPHNI 56
                                                                                                          SSLSPRQLLGFPCAEVSGLSTERVRELAVALAQKNVKLSTEQLRCLAHRLSEPPEDLDAL 116
                                                                                                                                                   MELKVFDQDLVTGDDP--VLSVLFDAGTLR----AGEFRRESFSLSPQGEGRLEVEFRL
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Lilly Corporate Center
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Strifler, Be
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                                                                                                                                                                                                                           Score 113.5; DB 3; Pred. No. 0.076; 2; Mismatches 257;
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                 -RFF-SRITKANVDLLPRGAPERQRLLPAALACWG 169
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                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Chiou, Xue-Chiou C. APPLICANT: Kramer, Ruth M. APPLICANT: Pickard, Richard T.
                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                                                           PRIOR APPLICATION DATA:
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                                                    APPLICATION NUMBER: US/08/827,208 FILING DATE: 28-MAR-1997
                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                             STREET: Lilly corporate indianapolis
                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                        STATE:
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                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----GYLVLDLSVQETLSGTPCL 609
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 3.5%; Score 113.5; DB Best Local Similarity 20.8%; Pred. No. 0.076; Matches 143; Conservative 72; Mismatches 2
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LENGTH: 913 amino acid
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                                                                             695 WRPLAQATHNFLRGLHFH--KDYFQHPHFSTW----KATTLD-----GLPNQLTPSE
                                                                                                                   539 --PLTVAEVQKLLGPHVEGLKAEERHRPVRDWILRQRQDDLDTLGLGLQGGIPN-----
                                                                                                                                                                                                                                                                                                                                                          384 KWNVTSLETLKALLEVDKGHEMSPQAP-----RRPLPQVATLIDRFVKGRGQLDKDTLDT 438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Gaylo, Paul J. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE:
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                                                                                                                                                           NLYAANLQDSLYWASEPSQFWDRWVRNQANLDKEQVPLLKIEEPPSTAGRIAEFFTDLLT 694
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                                                                                                                                                                                                 SEYFVKIQSFL--GGAPTE--DLKALSQQNVSMDLATFMKLR----
                                                                                                                                                                                                                                                                              LTAFYPGYLCSLSPEELSSVPPSSIWAVRPQDLDTCD--PRQLDVLYPKARLAF-QNMNG
PHECLEDVGYLI-----NTSCL 757
                                     -----GYLVLDLSVQETLSGTPCL 609
                                                                                                                                                                                                                                      LTTFEFGEWCEFSPYEVGF----PKYGAFIPSELFGSEFFMGQLMKRLPESRICFLEGIWS
                                                                                                                                                                                                                                                                                                                        --NLWALINEALLHDEPHDHKLSDQREALSHGQNPLPIYCAL----NTKGQ-----
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; TOPOLOGY: linear; MOLECULE TYPE: protein US-09-498-809-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Gaylo, Paul J.
REGISTATION NUMBER: 36,808
REFERENCE/DOCKET NUMBER: X-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 276-0756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS: LENGTH: 913 amino acids
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NAME: Gaylo, Paul J.
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APPLICATION NUMBER:
FILING DATE: 19-MAR-
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Eli Lilly and Company
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TITLE OF INVENTION: HUMAN PHOSPHOLIPASE A2 AND RELATED
TITLE OF INVENTION: NUCLEIC ACID COMPOUNDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
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417 LDGDLQEDEIPVVAIMATGGG-----IRAMTSLYGQLAGLKELGLLDCVSYITGA 460
                                        209 CPGPLDQDQQEAARAALQGGGPPYGPPSTWSVSTMDALRGLLPVLGQ----PIIRSIPQG
                                                                                   357 QVVRLVFPTSQEPLMRVELKKEAGLRELAVRLGFGPCAEEQAFLSRRKQVVAAALRQALQ 416
                                                                                                                                                                      299 HRVQLVV--PGSCEGPQEASVGTGTFRFHCPACWEQELSIRLQDAPEEQLKAPLSALPSG
                                                                                                                                                                                                                 117 PLDLLLFLNPDAFSGPQACT -----RFF-SRITKANVDLLPRGAPERQRLLPAALACWG
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chiou, Xue-Chiou C.
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19-MAR-1997
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                                                                                                                              -VRGSLLSEADVR-'---ALGGLACDLPGRFVAESAEVL---LPRLVS
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COUNTRY: USA
ZIP: 22040-0747

COMPUTER READABLE FORM.

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATER:
COMPUTER: IBM PC COMPATER:
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/426,819A
FILING DATE: 21-APR-1995
CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MUTPHY JI., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 230-107P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
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                                                                                                         TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
APPLICANT:
APPLICANT:
                 TOPOLOGY: no MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Hattori, Kunihiro TITLE OF INVENTION: Genes Coding TITLE OF INVENTION: Potentiator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               635
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Birch, Stewart, Kolasch & Birch
STREET: P.O. BOX 747
CITY: Falls Church
STATE: Virginia
                                                   STRANDEDNESS:
                                                                                             LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --PLTVAEVQKLLGPHVEGLKAEERHRPVRDWILRQRQDDLDTLGLGLQGGIPN-----
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5723318
                                                                         amino acid
                                                                                           33 amino acids
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Oh-Eda, Masayoshi
                                   not relevant
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peptide
NO
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OTHER INFORMATION:
OTHER INFORMATION:
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US-08-426-819A-18
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Search completed: December Job time: 706 sec
                                                                                            Query Match
Best Local Similarity
Matches 23; Conserv
                                                                                                                                                                                                                 FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FRAGMENT TYPE: N-terminal FEATURE:
                                                                                                                                                                                                                        NAME/KEY: Region LOCATION: 4..16 OTHER INFORMATION: OTHER INFORMATION:
                                                                 LOCATION: 1..13
OTHER INFORMATION:
OTHER INFORMATION:
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                                                     1 SRTLAGETGQEAAPLDGVLANPPXISXLXPRQL 33
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/note= "sequence (c)
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/note= "sequence a in Example
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          2001, 10:00:38
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Pred. No. 0.00055;
2; Mismatches 8
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Searched:
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                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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2: /cgn2_6/ptodata/2/paa/
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Gapop 10.0 , Gapext 0.5
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                                                      SUMMARIES
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1215.112 Million cell updates/sec
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No.	Score	% Query Match	% Query Match Length DB		ID	Description
1	3055	93.7	622	œ ¦	US-08-426-819-35	Sequence 35, Appl
2	2956	90.6	584	œ	US-08-426-819-36	Sequence 36, Appl
ω	1547	47.4	328	19	US-09-513-597-2	Sequence 2, Appli
4	1547	47.4	402	19	US-09-513-597-13	Sequence 13, Appl
υī	1531	46.9	399	19	US-09-513-597-1	Sequence 1, Appli
σ	1247	38.2	248	œ	US-08-426-819-37	Sequence 37, Appl
7	579.5	17.8	175	17	US-09-330-360-733	Sequence 733, App
œ	559	17.1	144	17	us-09-330-360-599	Sequence 599, App
9	482	14.8	122	17	US-09-330-360-702	Sequence 702, App

ALIGNMENTS

US-08-426-819-35
: Sequence 35, Application US/08426819
: GENERAL INFORMATION: APPLICATION NUMBER: US/08/426,819
FILING DATE: 21-APR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mulphy Jr., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 230-107P COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA: TITLE OF INVENTION: APPLICANT: Kojima, Tetsuo APPLICANT: Oh-Eda, Masayoshi APPLICANT: Hattori, Kunihiro CORRESPONDENCE ADDRESS: TELECOMMUNICATION INFORMATION: NUMBER OF SEQUENCES: APPLICANT: STREET: P.O. Box 70 CITY: Falls Church STATE: Virginia COUNTRY: ADDRESSEE: RY: USA 22040-0747 Yamaguchi, Nozomi Birch, Stewart, Kolasch & Birch O. Box 747 Genes Coding Potentiator : 37 for Megakaryocyte Version #1.30

TELEPHONE:

703-205-8000

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; TELEFAX: 703-205-8050
; INFORMATION FOR SEQ ID NO: 3
; SEQUENCE CHARACTERISTICS:
; LENGTH: 622 amino acids
TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-426-819-35
                                                                                                                                                            RESULT 2
US-08-426-819-36
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                                                                                                                                Sequence 36, Application US/08426819 GENERAL INFORMATION:
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Best Local Similarity 95.4%;
Matches 601; Conservative
                                                                                   APPLICANT:
APPLICANT:
                            APPLICANT: Hattori, Kunihiro TITLE OF INVENTION: Genes Coding TITLE OF INVENTION: Potentiator NUMBER OF SEQUENCES: 37
                CORRESPONDENCE
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                                                                                                                                                                                                                     DLLLFLNPDAFSGPQACTRFFSRITKANVDLLPRGAPERQRLLPAALACWGVRGSLLSEA 178
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                                                                                   Yamaguchi, Nozomi
Kojima, Tetsuo
Oh-Eda, Masayoshi
Birch,
                ADDRESS
 Stewart,
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 Kolasch & Birch
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LENGTH: 584 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; POPOLOGY: not relevant
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE: internal
US-08-426-819-36
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FILING DATE: 21-APR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MUTPHY Jr., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 2300
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8050
TELEPAX: 703-205-8050
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARROTERISTICS:
IFORMATION FOR SEQ ID NO: 36:
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Best Local Similarity
Matches 576; Conserv
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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CURRENT APPLICATION DATA:
                         517
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CITY: Fa
STATE: V
COUNTRY:
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                                                   LSQQNVSMDLATFMKLRTDAVLPLTVAEVQKLLGPHVEGLKAEERHRPVRDWILRQRQDD
                                                                                                                        LEVDKGHEMSPQAPRRPLPQVATLIDRFVKGRGQLDKDTLDTLTAFYPGYLCSLSPEELS
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LSQQNVSMDLATFMKLRTDAVLPLTVAEVQKLLGPHVEGLKAEERHRPVRDWILRQRQDD
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Pred. No. 1.7e-266;
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336 240

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US-09-513-597-13

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CURRENT APPLICATION NUMBER: US/09/513,597
CURRENT FILING DATE: 2000-02-25
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 328
TYPE: PAT
ORGANISM: Homo sapien
US-09-513-597-2
   APPLICANT: Scholler, Nathalle B.:
APPLICANT: Hellstrom, Ingegerd
APPLICANT: Hellstrom, Karl Erik
APPLICANT: Hellstorm, Karl Erik
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: CARCINOMAS
FILE REFERENCE: 730033.410
CURRENT APPLICATION UNMBER: US/09/513,597
CURRENT FILING DATE: 2000-02-25
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13
LENGTH: 402
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US-09-513-597-2
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Best Local Similarity
Matches 301; Conserva
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APPLICANT: Hellstom, Ingegerd
APPLICANT: Hellstorm, Karl Erik
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: CARCINOMAS
FILE REFERENCE: 730033.410
ORGANISM: Homo sapien
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97.18;
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Pred. No. 3.6e-135;
1; Mismatches 0;
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APPLICANT: Scholler, Nathalie B.
APPLICANT: Hellstrom, Ingegerd
APPLICANT: Hellstrom, Ingegerd
APPLICANT: Hellstrom, Karl Erik
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TITLE OF INVENTION: CARCINOMAS
FILE REFERENCE: 73003.410
CURRENT APPLICATION NUMBER: US/09/513,597
CURRENT FILING DATE: 2000-02-25
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 399
TYPE: PAT
ORGANISM: Homo sapien
US-09-513-597-1
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Best Local
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61 LDELYPQGYPESVIQHLGYLFLKMSPEDIRKWNVTSLETLKALLEVNKGHEMS------ 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity hes 301; Conserv
                                                                                                                                                                                                            Local Similarity
es 298; Conserv
                                                  FRREVEKTACPSGKKAREIDESLIFYKKWELEACVDAALLATQMDRVNAIPFTYEQLDVL
                                                                                                                                                        EVEKTACPSGKKAREIDESLIFYKKWELEACVDAALLATQMDRVNAIPFTYEQLDVLKHK
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                                                                                                                                                                                                       46.9%; milarity 97.1%; Conservative
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97.18;
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                                                                                                                                                                                                                     Score 1531; DB 19;
Pred. No. 1.6e-133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1547; DB 19;
Pred. No. 5.1e-135;
                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                                      DB 19;
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                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                      Query Match
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/426,819 FILING DATE: 21-APR-1995 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                      HYPOTHETICAL: FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: 703-205-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 3
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                    217
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                                                                                                                                                                                                                                                     Local Similarity
mes 242; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Birch, St. STREET: P.O. Box 747 CITY: Falls Church
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Murphy Jr., Gerald M
REGISTRATION NUMBER: 28,97:
REFERENCE/DOCKET NUMBER: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENGTH:
                 QQEAARAALQGGGPPYGPPSTWSVSTMDALRGLLPVLGQPIIRSIPQGIVAAWRQRSSRD 276
                                                                 RQRLLPAALACWGVRGSLLSEADVRALGGLACDLPGRFVAESAEVLLPRLVSCPGPLDQD 216
                                                                                                                                 EQLRCLAHRLSEPPEDLDALPLDLLLFLNPDAFSGPQACTRFFSRITKANVDLLPRGAPE 156
RQRLLPAALACWGVRGSLLSEADVRALGGLACDLPGRFVAESAEVLLPRLVSCPGPLDQD 180
                                                                                                                  EQLRCLAHRLSEPPEDLDALPLDLLLFLNPDAFSGPQACTRFFSRITKANVDLLPRGAPE 120
                                                                                                                                                                                  GETGQEAAPLDGVLANPPNISSLSPRQLLGFPCAEVSGLSTERVRELAVALAQKNVKLST 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       248 amino acids
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                                                                                                                                                                                                                                                     Conservative
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Oh-Eda, Masayoshi
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                                                                                                                                                                                                                                                                                                                                                                                                        not relevant
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97.6%;
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Pred. No. 2.6e-107;
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SOFTWARE: PAST
SEQ ID NO 733
FRIGHH: 175
                                                                                                                                                                                                                                Sequence 599, Application US/09330360 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 733, Application US/09330360 GENERAL INFORMATION:
                                                                                                                                                                      APPLICANT:
APPLICANT:
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Best Local Similarity
Matches 129; Conserv
                                                                           FILE REFERENCE: MLN98-34pA
CURRENT APPLICATION NUMBER: US/09/330,360
CURRENT FILING DATE: 1999-06-11
PRIOR APPLICATION NUMBER: 60/090,258
PRIOR FILING DATE: 1998-06-22
NUMBER OF SEQ ID NOS: 1102
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                               APPLICANT: Robison, Keith E.
APPLICANT: Holtzman, Douglas A.
TITLE OF INVENTION: Nucleic Acid Molecules Derived
TITLE OF INVENTION: Human Fetal Lung Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/330,360 CURRENT FILING DATE: 1999-06-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Holtzman, Douglas A.
TITLE OF INVENTION: Nucleic Acid Molecules Derived from
TITLE OF INVENTION: Human Fetal Lung Library
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NUMBER OF SEQ ID NOS:
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TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: SIGNAL
LOCATION: (1)...(33)
NAME/KEY: VARIANT
LOCATION: (1)...(175)
COTHER INFORMATION: Xaa = Any Amino
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                                                                                                                                                                                                                                                                                                                                                 166 SGLWGVRG 173
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                                                                                                                                                                                                          Gearing, David P.
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Pred. No. 3.8e-45;
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SEQ ID NO 599

TYPE: PRT LENGTH:

144

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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(33)
; NAME/KEY: VARIANT
; LOCATION: (1)...(144)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-330-360-599
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                                                                                                                                                                                                                                                                         ; NAME/KEY: SIGNAL ; LOCATION: (1)...(33) US-09-330-360-702
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Best Local Similarity 86.0%;
Matches 117; Conservative
                                                                                                                                                                                                          Query Match
Best Local (
                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 702
                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: MLN98-34PA
CURRENT APPLICATION NUMBER: US/09/330,360
CURRENT FILING DATE: 1999-06-11
PRIOR APPLICATION NUMBER: 60/090,258
PRIOR FILING DATE: 1998-06-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Holtzman, Douglas A.
TITLE OF INVENTION: Nucleic Acid Molecules Derived from
TITLE OF INVENTION: Human Fetal Lung Library
FILE REFERENCE: MLN98-34PA
                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                LENGTH: 122
TYPE: PRT
ORGANISM: Homo sapiens
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121 D 121
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                                                             61
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                                                                                                                                                                                           Local Similarity 84.3 es 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 LSPRQLLGFPCAEVSGLSTERVRELAVALAQKNVKLSTEQLRCLAHRLSEPPEDLDALPL 120
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                                                                                                                                           1 MALQRLDP-CWSCGDRP-GSLLFLLFSLGWVHPARTLAGETGTESAPLGGVLTTPHNISS 58
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                                                           LSPRQLLGFPCAEVSGLSTERVRELAVALAQKNVKLSTEQLRCLAHRLSEPPEDLDALPL 118
                            D 119
                                                                                                                            MALPTARPLLGSCGTPALGSLLFLLFSLGWVQPSRTLAGETGQEAAPLDGVLANPPNISS 60
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                                                                                                                                                                                                         14.8%;
84.3%;
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Pred. No. 2.2e-43;
2; Mismatches 15;
                                                                                                                                                                                         Score 482; DB 17;
Pred. No. 2.7e-36;
2; Mismatches 15;
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                                                                                                                                                                                                                        Length 122;
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WESULT 11
US-08-426-819-33
Sequence 33, Application US/08426819
GENERAL INFORMATION:
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Best Local Similarity
~~+~hes 93; Conserva
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CURRENT FILING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/180,628
PRIOR APPLICATION NUMBER: 60/180,628
PRIOR FILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 520
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NAME/KEY: SITE
LOCATION: (127)
OTHER INFORMATION: >
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PM041
                                                                 APPLICANT: Oh-Eda, Ma
APPLICANT: Hattori, K
TITLE OF INVENTION: G
TITLE OF INVENTION: P
NUMBER OF SEQUENCES:
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ORGANISM: Homo
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APPLICANT:
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LOCATION: (117
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LOCATION: (131
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                                    CORRESPONDENCE ADDRESS: ADDRESSEE: Birch, St
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                     STREET:
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SEE: Birch, Stewart, Kolasch & Birch P.O. Box 747
Falls Church
                                                                                 Kojima, Tetsuo
Oh-Eda, Masayoshi
Hattori, Kunihiro
NVENTION: Genes Coding !
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COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk

Virginia RY: USA 22040-0747

COUNTRY:

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US-09-758-458-404
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; MOLECULE TYPE:
US-08-426-819-33
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CURRENT FILING DATE: 2001-01-11
                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 520
                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: PM041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Ver. 2.0
                                                                OTHER INFORMATION: Xaa
NAME/KEY: SITE
LOCATION: (137)
OTHER INFORMATION: Xaa
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                          NAME/KEY: SITE
LOCATION: (140)
                                                                                                                                                      NAME/KEY: SITE
LOCATION: (128
                                                                                                                                                                                                                 ORGANISM: Homo sapiens
                                                                                                                                                                                                                                            LENGTH: 144
TYPE: PRT
                                                                                                                                                                                                      FEATURE:
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LENGTH: 65 amino acids
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FILING DATE: 21-APR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald M.
REGISTRATION NUMBER: 28,977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: 703-205-8000
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SOFTWARE: PatentIn Release #1.0, Version #1.30
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                                                                                                                                Xaa equals any of the naturally occurring L-amino acids
                                                                equals any of the naturally occurring L-amino acids
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RESULT 13
US-08-426-819-19
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ZIP: 22040-074,
ZIP: 22040-074,
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: BM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: TEM PC COMPATIBLE
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald
REGISTRATION NUMBER: 28,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA: US/08/426,819
                                   FEATURE:
                                                                                              NAME/KEY: Peptide LOCATION: .1..40 OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                          IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                             HYPOTHETICAL: NO FRAGMENT TYPE: in
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TELECOMMUNICATION TMECTOR
TELECOMOUNICATION TMECTOR
TELECOMOUNICATION TMECTOR
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NAME/KEY: Modified-site
                                                                  OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39 TGTESAPLGGVLTTPHNISSLSPRQLLGFPCAEVSGLSTERVRELAVALAQKNVK-LSTE 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 QRLDPCW----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QL 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58;
                                                                                                                                                                                                                                                                          нрсү5
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WENTION: Genes Coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kojima, Tetsuo
Oh-Eda, Masayoshi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                not relevant
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O. Box 747
                                                                                                                                                                                                                                                                                                                                             internal
                                                                                                                                                                                                                                                                                                                                                                                                            peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   not relevant
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47.5%;
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                                                               /label= fragment /note= "sequence of cyanogen bromide fragment of MegPOT fr cDNA in Table 3" \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          230-107P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 220; DB 21;
Pred. No. 1.1e-11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #1.30
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OTHER INFORMATION:

/product= "is Xaa in COS"

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COCATION: 1.16
COTHER INFORMATION:
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COTHER INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 230-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
                                CLONE:
                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Birch, Stev
STREET: P.O. Box 747
CITY: Falls Church
STATE: Virginia
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                                                                           MOLECULE TYPE: POPE NOTHETICAL: NO FRAGMENT TYPE: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Genes Coding for Megakaryocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            244 DALRGLLPVLGQPIIRSIPQGIVAAWRQRSSRDPSWRQPE 283
                                                           MMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY:
NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/426,819 FILING DATE: 21-APR-1995 CLASSIFICATION: 435
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LOCATION:
                                                                                                                                   TYPE: amino
STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
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                                                                                                                        TOPOLOGY:
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                                                                                                                                                                   ENGTH:
                                                                                                                                                     amino acid
                                                HPCY5
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Oh-Eda, Masayoshi
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                                                                                                                        not relevant
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Peptide
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                                                                           internal
                                                                                                      peptide
                                                                                                                                        not relevant
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y 100.0%; Pr
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/note= "sequence of cyanogen bromide fragment representing
C-terminus of MegPOT determined in Example 28"
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Pred. No. 1.1e-11;
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CURRENT FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: 09/577,408
PRIOR FILING DATE: 2000-05-18
PRIOR FILING DATE: 2000-05-18
NUMBER OF SEO ID NOS: 16102
SOFTWARE: CUSTOM
SEO ID NO 10981
LENGTH: 824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 10981, Application PC/TUS0114827
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND
FILE REFERENCE: 21272-104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best
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Best Local Similarity 23.3%;
Matches 155; Conservative 70
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LOCATION: (747)...(768)

OTHER INFORMATION: by eMATRIX, accession number PR00500B, p-value-4.316e-09, raw
OTHER INFORMATION: score of 7.74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                              194 RPGTFGALGALATLNLAHNALVYLPAMAFQGLLRVRWLRLSHNALSVLAPEALAGLPALR 253
                                                                             415 RAVAGPRAPPRGPPRGPGEERAVAPCPRACVCVPESRHSSCEGCGLQAVPRGF-----
                                                                                                                                                         363 RPLLEW-----LARARVRSDG--ACQGPRRLRGEALDALRPWDLRCPGDAAQEEEELEE 414
                                                                                                                                                                                                                                     306 DGGALQALGPRAFA---HCPRLHTLDLRGNQLDTLPPLQGPGQLRRLRLQGNPLWCGCQA 362
                                                                                                                                                                                                                                                                                                                  254 RISLHHNELQALPGPV------LSQARGLARLELGHNPLTYAGEEDGLALPGLRELLL
                                                                                                                  223 AALQG-----GGPPYGPPSTWSVSTMDALRGLLPVLGQPI-----IRSIPQGIVAAWRQR 272
                                                                                                                                                                                                                                                                                                                                           72 VSGLSTERVRELAVALAQKNVKLSTEQLRCLAH-RLSEPP-----EDLDALP--LDLLL 122
                                                                                                                                                                                                                                                                                                                                                                                                                                   15 RPGSL--LFLLFSLGWVHPARTLAGETGTESAPLGGVLTTPHN-ISSLSPRQLLGFPCAE 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83 LAVALAQKNVKLSTEQLRCLAHRLSEPPEDLDALP 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match 5.0%;
Local Similarity 97.1%;
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OTHER INFORMATION:
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                                    SSRDPSWRQPERTILRPRERREVEKTACPSGKKAREIDESLIFYKKWELEACVDAALLAT 332
                                                                                                                                                                             -----WGVRGSLLSEADVRALGGLACDLPGRFVAESAEVLLPRLVSCPGPLDQDQQEAAR
                                                                                                                                                                                                                                                                       -----FLNPDAFSGPQACTRFFSRITKAN-VDLLP----RGAPERQRLLPAALAC---- 167
----PS--DTQLLDLRRNHFPSVPRAAFP------GLGHLVSLHLQHCGIAELEAG
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/note= "region of
codons."
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Pred. No. 0.0063;
0; Mismatches 267
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Pred. No. 2.3e-07;
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Search completed: December 7, 2001, 09:52:20 Job time: 248 sec

Run

Compugen Ltd

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Result
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Maximum
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Listing first 45 s
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       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/1/paa/P

2: /cgn2_6/ptodata/1/paa/U

3: /cgn2_6/ptodata/1/paa/U

4: /cgn2_6/ptodata/1/paa/U

5: /cgn2_6/ptodata/1/paa/U

6: /cgn2_6/ptodata/1/paa/U
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length: 2000000000
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Match
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Gapop 10.0 , Gapext 0.5
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3261
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     GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
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/cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep:*
/cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep:*
/cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:*
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US-09-828-792-733
US-09-828-792-792
US-09-828-792-702
US-09-815-242-11089
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US-09-815-242-11925
US-09-815-242-11925
US-09-722-708-55
US-09-722-708-55
US-09-657-440-2
US-60-325-795-4
US-09-981-353-188
US-09-981-353-188
US-09-815-242-11062
US-09-815-242-11062
US-09-815-242-12811
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                            Sequence 733, App Sequence 799, App Sequence 702, Appli Sequence 5064, App Sequence 11925, A Sequence 11925, A Sequence 2, Appli Sequence 2, Appli Sequence 44, Appli Sequence 44, Appli Sequence 188, Appli Sequence 187, Appli Sequence 5107, Appli Sequence 5117, Appli Sequence 5111, Appli Sequence 5111, Appli Sequence 1149, Appli Sequence 51, Appli Sequence 51, Appli Sequence 51, Appli Sequence 12490, Appli Sequence 5155, Appli Sequence 5168, Appli Sequence 6555, Appli Sequence 6585, Appli Sequence 65855, Ap
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US-09-828-792-733
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ALIGNMENTS

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FEATURE:

; NAME/KEY: SIGNAL

; LOCATION: (1)...(33)

; NAME/KEY: VARIANT

; LOCATION: (1)...(175)

; OTHER INFORMATION: Xaa - A
US-09-828-792-733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Gearing, David P.
APPLICANT: Robison, Keith E.
APPLICANT: Holtzman, Douglas A.
TITLE OF INVENTION: Nucleic Acid Molecules Derived fro
TITLE OF INVENTION: Human Fetal Lung Library
FILE REFERENCE: MLN98-34Pa
CURRENT APPLICATION NUMBER: US/09/828,792
CURRENT FILING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: US/09/330,360
PRIOR FILING DATE: 1999-06-11
PRIOR FILING DATE: 1999-06-11
PRIOR APPLICATION NUMBER: 60/090,258
PRIOR FILING DATE: 1998-06-22
NUMBER OF SEQ ID NOS: 1102
SOPTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 733
LENGTH: 175
В
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                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 129; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
                                                                                                                       119
                                      168 --- WGVRG 172
                                                                                 121
166 SGLWGVRG 173
                                                                                                                                                                                                        59
                                                                                                                                                              61 LSPRQLLGFPCAEVSGLSTERVRELAVALAQKNVKLSTEQLRCLAHRLSEPPEDLDALPL
                                                                                                                                                                                                                                          DLLLFLNPDAFSGPQA---
                                                                                                            DLLLFLNPDAFSGPQACTRFFSRITKANVDLLPRGAPERQRLL-------PAALAC- 167
                                                                                                                                                                                     LSPRQLLGFPCAEVSGLSTERVRELAVALAQKNVKLSTEQLRCLAHRLSEPPEDLDALPL
                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                               17.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Any Amino
                                                                                                                                                                                                                                                                                                                         Score 579.5; DB 5; Pred. No. 2.4e-42; 5; Mismatches 23;
                                                                               ---XPVSSPASRRPMWTCSEGGSRATAAAACG 165
                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                  Length 175;
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US-09-828-792-599

Sequence

Application US/09828792

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                                                       SEQ ID NO 702
LENGTH: 122
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                           Sequence 702,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: SIGNAL
LOCATION: (1)...(33)
NAME/KEY: VARIANT
LOCATION: (1)...(144)
OTHER INFORMATION: Xaa = Any Amino Acid
-09-828-792-599
                                                                                         PRIOR APPLICATION NUMBER: 60/090,258
PRIOR FILING DATE: 1998-66-22
NUMBER OF SEQ ID NOS: 1102
SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/828,792
CURRENT FILING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: US/09/330,360
PRIOR FILING DATE: 1999-06-11
                                                                                                                                                                                                                                         APPLICANT: Holtzman, Douglas A.
TITLE OF INVENTION: Nucleic Acid Molecules Derived from
TITLE OF INVENTION: Human Fetal Lung Library
FILE REFERENCE: MLN98-34Pa
                                                                                                                                                                                                                                                                                                           APPLICANT: Gearing, David P. APPLICANT: Robison, Keith E APPLICANT: Holtzman, Dougla.
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PRIOR FILING DAYE: 1999-06-11
PRIOR APPLICATION NUMBER: 60/090,258
PRIOR FILING DAYE: 1998-06-22
NUMBER OF SEQ ID NOS: 1102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Gearing, David P.
APPLICANT: Robison, Keith E.
APPLICANT: Holtzman, Douglas A.
TITLE OF INVENTION: Nucleic Acid Molecules Derived
TITLE OF INVENTION: Human Fetal Lung Library
FILE REFERENCE: MLN98-34Pa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/828,792
CURRENT FILING DATE: 2001-04-09
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ for Windows Version 3.0
                 ORGANISM: Homo sapiens
                                       TYPE: PRT
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DLLLFLNPDAFSGPQA 134
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                                                                                                                                                                                                                                                                                                                               Robison, Keith E.
                                                                                                                                                                                                                                                                                                                                                                                           Application US/09828792
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86.0%;
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Pred. No. 9.9e-41;
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; TITLE OF INVENTION: NOVEL SECRETED PROTEINS AND FILE REFERENCE: P-14990
; CURRENT APPLICATION NUMBER: US/60/325,795
; CURRENT FILING DATE: 2001-09-28
; NUMBER OF SEO ID NOS: 10
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 2
; ELENGTH: 762
; TYPE: PAT
; ORGANISM: Homo sapiens
US-60-325-795-2
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; LOCATION: (1)...(33)
US-09-828-792-702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-60-325-795-2
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Best Local Similarity
Matches 102; Conserv
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APPLICANT: Wang, He
APPLICANT: Zhi, Yu
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                                                                                                                                                    371 RAVAGPRAPPRGPPRGPGEERAVAPCPRACVCVPESRHSSCEGCGLQAVPRGF-----
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468 ALAGLGRLIYLYLSDNQLAGLSAAALEGAPR--
                                                                                                                                                                                      223 AALQG-----GGPPYGPPSTWSVSTMDALRGLLPVLGQPI----IRSIPQGIVAAWRQR 272
                                                                                                                                                                                                                                                                                                                                                                                      210 RLSLHHNELQALPGPV------LSQARGLARLELGHNPLTYAGEEDGLALPGLRELLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15 RPGSL--LFLLFSLGWVHPARTLAGETGTESAPLGGVLTTPHN-ISSLSPRQLLGFPCAE 71
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nes 113; Conser
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                                                                           ----PS--DTQLLDLRRNHFPSVPRAAFP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LSPRQLLGFPCAEVSGLSTERVRELAVALAQKNVKLSTEQLRCLAHRLSEPPEDLDALPL 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MALPTARPLIGSCGTPALGSLLFLLFSLGWVQPSRTLAGETGQEAAPLDGVLANPPNISS
                                   QMDRVNAIPFTY - - - EQLDVLKHKLDELYPQGYPESVIQHLGYLFLKMSPEDIRKWNVTS
                                                                                                               SSRDPSWRQPERTILRPRFRREVEKTACPSGKKAREIDESLIFYKKWELEACVDAALLAT
                                                                                                                                                                                                                                RPLLEW---
                                                                                                                                                                                                                                                                                                           DGGALQALGPRAFA----HCPRLHTLDLRGNQLDTLPPLQGPGQLRRLRLQGNPLWCGCQA 318
                                                                                                                                                                                                                                                                                                                                                 -----FLNPDAFSGPQACTRFFSRITKAN-VDLLP----RGAPERQRLLPAALAC----
                                                                                                                                                                                                                                                                                                                                                                                                                            VSGLSTERVRELAVALAQKNVKLSTEQLRCLAH-RLSEPP-----EDLDALP--LDLLL 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                RPGTFGALGALATLNLAHNALVYLPAMAFQGLLRVRWLRLSHNALSVLAPEALAGLPALR 209
                                                                                                                                                                                                                                                                   ----WGVRGSLLSEADVRALGGLACDLPGREVAESAEVLLPRLVSCPGPLDQDQQEAAR 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Application US/60325795
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.0%; Score 131.5; DB 24.4%; Pred. No. 0.0028; tive 45; Mismatches 18
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Pred. No. 2.8e-34;
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                                                                         -GLGHLVSLHLQHCGIAELEAG
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US-09-815-242-11089
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SEQ ID NO 11089
LENGTH: 1159
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Best Local Similarity 20.28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
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TITLE OF INVENTION: Identification of Essential
TITLE OF INVENTION: Prokaryotes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/191,078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Haselbeck, Robert
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                                                                                                                                                                                                           189 DLPGRFVAESAEVLLPRL-----VSCPGPLDQDQQEAA-RAALQGGGPPYGPPSTWSVST 242
                                                                                                                                                                                                                                                                                                                                                                                                                           495 INMARKLEGVTRNAGKHAGGVVISPTLITDFAPLYCDNEGLHPVTHFDKNDVEYAGLVKF 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OR FILING DATE: 2000-05-26

OR APPLICATION NUMBER: 60/242,578

OR FILING DATE: 2000-10-23

OR APPLICATION NUMBER: 60/253,625

OR FILING DATE: 2000-11-27

OR APPLICATION NUMBER: 60/257,931

OR APPLICATION NUMBER: 60/257,931

OR APPLICATION NUMBER: 60/257,931
                                                                                                                                                                                                                                                                                                                                                                            71 EVSGLSTERVRELAVALAQKNVKLSTEQLRCLAHRLSEPPEDLDALPLDLLLFLNPDAFS 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29 VHPARTLAGETGTESAPLGGVLTTPHNISSLSPR------QLLGFPCA 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/269,308
                                                                                                                                                                   FRPGPLQSGMVDNFIDRKHGREEVSYP---DAEYQHASLKPILE---PTYG-----
                                                                                                                                                                                                                                                                                                                                           DFLGLRTLTIIKWALDII--NVRMVRE------GKPRVDIAAIPLD-----DPESFE 598
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NGIDGELSMKIFDLVEKFAGYGFNKSHSAAYALVSYQTLWLKTHFPAEFMAAVMTSEMDN 793
                                                                                                                       MDALRGLLPVLGQPIIRSIPQGIVAAW------RQRSSRDPSWRQPERTILRPRFRR
                                                                                                                                                                                                                                                       LLKRSETTAVFQLESRGMKDLIKRLQPD------CF-----EDIIAL--VAL
                                                                                                                                                                                                                                                                                               --GPQACTRFFSRITKANVDLLPRGAPERQRLLPAALACWGVRGSLLSEADVRALGGLAC 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   149;
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Trawick, John D.
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Zyskind, Judith W.
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                                                                             ---IILYQEQVMQIAQ-VLAGYTLGGADLLRRAMGKKKPEEMAKQRLVFKEGAEK 733
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                      ORGANISM: Pseudomonas aeruginosa US-09-815-242-5064
                                                                                                                                                                         NUMBL.. SOFTWARE: Fasts SOFTWARE: Fasts SEQ ID NO 5064
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GENERAL INFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,
CURRENT FILING DATE: 2001-03-21
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TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
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                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 2000-12-22
                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/253,625 PRIOR FILING DATE: 2000-11-27
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                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/257,931
                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/207,727
                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 2000-10-23
                                                                                                                                                                  LENGTH: 2
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VKSLAISLSEHQITPSFIKQFKALLEPVSGGTLPINVYYQSPKGRALLRLGVQWSIIPT- 1138
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                                                                                                                                                                                                                                FastSEQ
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Yamamoto, Robert T.
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21.7%; Pre
21.7%; 70;
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Query Match 3.1 Best Local Similarity 21.7 Matches 138; Conservative

Score 101.5; D Pred. No. 5.6; 70; Mismatches

DB 5; 216;

Indels 211; Length 2472;

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APPLICANT: Xu, H. HOWARD
TITLE OF INVENTION: Identification of Ess
FILE REFERENCE: ELLTRA, 011A
CURRENT APPLICATION NUMBER: US/09/815,24:
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/21,078
PRIOR FILING DATE: 2000-03-21
PRIOR PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/243,578
PRIOR APPLICATION NUMBER: 60/243,525
PRIOR APPLICATION NUMBER: 60/243,525
PRIOR FILING DATE: 2000-11-27
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US-09-815-242-11925
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIWAVRPQDLDTCDPRQLDV----LYPKARLAFQNMNGSEYFVKIQSFLGGAPTEDLKAL 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GHPSELDALLAPLKQIADTL--AVLGFGQPRKVILDQLDV----------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HQLVIKEARNGLEQAKDAIIEFIASQWNHEHLARVPELLTQVRGGLAMIPLERAATLLET 496
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LGGLL-----RKLRQTQQMALVGLLR-----NQDVATSLGYLARVYARLEGLCREAPLGP 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11925, Application US/09815242
                                                                                                                                                                                                                                                                                                                                                                                                                  Ohlsen, Kari L.
Zyskind, Judith W.
                                                                                                                                                                                                                                                                                                                                                                           Wall, Daniel
Trawick, John D.
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PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEO ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.
SEQ ID NO 11925
LENGTH: 956
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US-09-722-487-55
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US-09-815-242-11925
                                                                                      Sequence 55, Application US/09722487
GENERAL INFORMATION:
APPLICANT: Hockensmith, Joel W.
Muthuswami, Rohini
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Best Local Similarity
Matches 142; Conserv
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                                                                                                                                                                                                                                       759
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                                 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TARGETING DNA METABOLIC PROPERTY AMINOGLYCOSIDE DERIVATIVES
CORRESPONDENCE ADDRESS:
                    NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                               APDLATQEAEYRRVLDALDGRPLVARTLDVGGDKPLPYWPIPHEENPYLGLRGIRLTLQR
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                                                                                                                                                                                                                                                                                                                                                                                    AQRLEPART - - RDGHAVEVCANLGDTAGAARAVELGAEGVGLLRTEFVFMNN - - - -
                                                                                                                                                                                                                                                                                                                                                                                                                      SWR-QPERTILRPRFRREVEKTACPSGKKAREID-----ESLIFYKKWELEACVD 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                          LGIPALVGAGAAVLGLEPGTALLLDGEHGWLQV--APSTEQLQQAAAERDARQQRQARAD
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ilarity 22.0%;
Conservative 4
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Pred. No. 1
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TOPOLOGY: linear;

MOLECULE TYPE: peptide;
SEQUENCE DESCRIPTION: S
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Best Local Similarity 20.88;
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INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 941 amino acids
TYPE: amino acid
STRANDEDNESS: single
                       377
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                                                                                                                                             269
                                                                                                                                                                                                                                                                     240 VSTMDALRGLLP-----
                                                                                                                                                                                                                                                                                                           149 GHPQASLETQSTPFANTTHEPLRKVKNFQETAASSSGQPPRDPELEARIGRPSTSGQNIS
                                                                                                                                                                                                                                                                                                                                                                                           115 RPPNQVTVAGISLPLANSPPGVPSQQ------LWG
                                                                                                                                                                                                                                                                                                                                                                                                                                 139 F--SRITKANVDL----LPRGAPERORLLPAALACWGVRGSLLSEADVRALGGLACDL-P 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   114 DALPLDL----LLF--------LNPDAF-------SGPQACTRF 138
                                                                                                                                                                                                                          209 GSVMPRTEGRLQQKAGTPMHRVVGSQQGRCIRNGERFQVKIGYNEALIAVFKSLPSRSYD
                                                                                                                                                                                                                                                                                                                                                192 GRFVAESAEVLLPRLVSCPGPLDQDQQEAARAALQGGGPPYGP------PST----WS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58 SLSPRQLLGFPCAEVSGLSTERVRELAV----ALAQKNVKLSTEQLRCLAHRLSEPPEDL 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55 PRDPSKSGSHGIFFKQQNPSSSSHGDQRPQNPHSFPPNTSEQAKGMWQRPEEMPTACPSY 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 SISP---LKCPCL----LQRSRGKKIEANRQKALARRAEKLLAEQHQKPAQSKQGPSQNL 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/09/722,487
ETLING DATE: 28-Nov;2000
CLASSIFICATION: -(Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 9426-005-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)7990900
TELEPAX: (212)8699741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                 P---SW------RQPERTILRPRERRE--VEKTACPSGKKAREIDESLIFY 316
                 MSPEDIRKWNVTS-----LETLKALLEVDKGHEMSPQAPRRPLPQVATLIDRFVKGRGQ 430
                                                         AKTGLPAAPSLAFVKGQCVLISRARF---EADI------SYSEDLIA----LFKQ 358
                                                                                                  KKWELEACVDAALLATQMDRVNAIPFTYEQLDVLKHKLDELYPQGYPESVIQHLGYLFLK 376
                                                                                                                                           PATKTWNFSMTDYGPLMKAAQRLPGIT-LQPLEGAEGHMESPSTSSG------II 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: PENNIE & EDMONDS LLP STREET: 1155 Avenue of the Americas CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 09/179,558
FILING DATE: <UNKNOWN>
APPLICATION NUMBER: U.S. 60/063,898
FILING DATE: 31-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IBM Compatible
                                                                                                                                                                                                                                                                 -VLGQPIIRSIPQG-----IVAAWRQRSSR--D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO: 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 99.5;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         216; Indels 263;
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=
                                                                                                                                                                                                                                                                                                                                                                                           ----CELGQ 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                          268
                                                                                                                                                                                                                                                                   276
                                                                                                                                                                                                                                                                                                           208
                                                                                                                                                                                                                                                                                                                                                  239
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RESULT 9
US-09-722-708-55
Sequence 55, Application US/09722708
GENERAL INFORMATION:
; MOLECULE TYPE: peptide;
; SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-722-708-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Š
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                                                                                                                                                                                TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: 55:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FBASESQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/09/722,708
FILING DATE: 28-Nov-2000
CLASSIFICATION: CUBROWN>
PRIOR APPLICATION: CUBROWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    551 --FLKNIKTAVCAAMP----LLKVAKRVILLSGTPAMSRPAELYTQILAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            503 NPLDINV-VVTGKDRLTDGLVNIVSFDLLSKLEKQLKPPFKVVIIDESH------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    443 NFAIAQRGRLLLADDMGLGKTIQAICIAAYYRKEWPLLVVVPSSVRFTWEQAFCRWLPSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             485 -----KARLAFQNMNG------SEYFVKIQSFLGGAPTED------LKAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  431 LDKDTLDTLTAFYPGYLCSLSPEELSSVPPSSIWAVRPQDLDTCDPRQLDVLYP----- 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             574 QDDLDTLGLGLQGGIPNGYLVLDLSVQE-TLSGTPCLLGPGPVLT-VLAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  359 M---DSRKYDVKTRKWSFLLEEYSKLMERVRG---PPQVQLDPLPKTLTLF-----RAQ 406
                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 9426
TELECOMMUNICATION INFORMATION:
TELLEPHONE: (212)7909990
TELEFAX: (212)78699741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Muthuswami, Robini
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TARGETING DNA METABOLIC PROCESSES USING
AMINOGLYCOSIDE DERIVATIVES
                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Hockensmith, Joel W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SQQNVSMDLATFMKLRTDAVLPLT----VAEVQKLLGPHVEGLKAEERHRPVRDWILRQR 573
                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: U.S. FILING DATE: 31-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 1155 A
                                                                                                               TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 09/179,558 FILING DATE: <Unknown>
                                                                                     STRANDEDNESS: single
                                                                                                                                     LENGTH: 941 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---TSLSP--VADIPEA-----DLSRVDSKLVSSLLPFQRAGV 442
                                                                                                                                                                                                                                                                                                  9426-005-999
                                                                                                                                                                                                                                                                                                                                                                                                                  60/063,898
                       55
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Query Match
Best Local Similarity

3.1%;

Score 99.5; Pred. No. 2; Mismatches

DB 5; 216;

Length 941; Indels 263;

Gaps

40;

Matches

148;

Conservative

83;

```
; TYPE: PRT; ORGANISM: Streptomyces venezuelae US-09-657-440-2
                                                                                                    APPLICANT: McDANIEL, Robert
APPLICANT: TANG, Li
APPLICANT: TANG, Li
TITLE OF INVENTION: RECOMBINANT NARBONOLIDE PO
FILE REFERENCE: 300622002120
CURRENT APPLICATION NUMBER: US/09/657,440
CURRENT FILING DATE: 2000-09-07
PRIOR APPLICATION NUMBER: 09/320,878
PRIOR FILING DATE: 1999-05-27
PRIOR FILING DATE: 1999-05-27
PRIOR APPLICATION NUMBER: CIP OF 09/141,908
PRIOR FILING DATE: 1998-08-28
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 10
US-09-657-440-2
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                                                              SEQ ID NO 2
LENGTH: 3739
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/09657440 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                              APPLICANT: ASHLEY, Gary
APPLICANT: BETLACH, Melanie C..
APPLICANT: BETLACH, Mary C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   551 --FLKNIKTAVCAAMP----LLKVAKRVILLSGTPAMSRPAELYTQILAV 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NPLDINV-VVTGKDRLTDGLVNIVSFDLLSKLEKQLKPPFKVVIIDESH------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NFAIAQRGRLLLADDMGLGKTIQAICIAAYYRKEWPLLVVVPSSVRFTWEQAFCRWLPSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LQK-----TSLSP--VADIPEA-----DLSRVDSKLVSSLLPFQRAGV 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LDKDTLDTLTAFYPGYLCSLSPEELSSVPPSSIWAVRPQDLDTCDPRQLDVLYP----- 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               M---DSRKYDVKTRKWSFLLEEYSKLMERVRG---PPQVQLDPLPKTLTLF-----RAQ 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MSPEDIRKWNVTS-----LETLKALLEVDKGHEMSPQAPRRPLPQVATLIDRFVKGRGQ 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AKTGLPAAPSLAFVKGQCVLISRARF---EADI-----SYSEDLIA----LFKQ 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KKWELEACVDAALLATOMDRVNAIPFTYEQLDVLKHKLDELYPOGYPESVIOHLGYLFLK 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PATKTWNFSMTDYGPLMKAAQRLPGIT-LQPLEGAEGHMESPSTSSG------II 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GSVMPRTEGRLQQKAGTPMHRVVGSQQGRCIRNGERFQVKIGYNEALIAVFKSLPSRSYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VSTMDALRGLLP-----VLGQPIIRSIPQG-----IVAAWRQRSSR--D 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GHPQASLETQSTPFANTTHEPLRKVKNFQETAASSSGQPPRDPELEARIGRPSTSGQNIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GRFVAESAEVLLPRLVSCPGPLDQDQQEAARAALQGGGPPYGP-----PST----WS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RPPNQVTVAGISLPLANSPPGVPSQQ------LWG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F--SRITKANVDL----LPRGAPERQRLLPAALACWGVRGSLLSEADVRALGGLACDL-P 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRDPSKSGSHGIFFKQQNPSSSSHGDQRPQNPHSFPPNTSEQAKGMWQRPEEMPTACPSY 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DALPLDL----LLF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SISP---LKCPCL----LQRSRGKKIEANRQKALARRAEKLLAEQHQKPAQSKQGPSQNL 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SLSPRQLIGFPCAEVSGLSTERVRELAV----ALAQKNVKLSTEQLRCLAHRLSEPPEDL 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SQQNVSMDLATFMKLRTDAVLPLT----VAEVQKLLGPHVEGLKAEERHRPVRDWILRQR 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----KARLAFQNMNG-----SEYFVKIQSFLGGAPTED-----LKAL 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----LNPDAF------SGPQACTRF 138
                                                                                                                                                                                                                                                                                                        POLYKETIDE
                                                                                                                                                                                                                                                                                                        SYNTHASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----CELGQ 148
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RESULT 11

US-60-325795-4

US-60-325795-4

Sequence 4, Application US/60325795

GENERAL INFORMATION:

APPLICANT: Su, Eric W

APPLICANT: Zhi, Yu

PITLE OF INVENTION: NOVEL SECRETED PROTEINS ANI

FILE REFERENCE: P-14990

CURRENT APPLICATION NUMBER: US/60/325,795

CURRENT FILING DATE: 2001-09-28
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                                                                                                                                                                                          ; TYPE: PRT; ORGANISM: Homo sapiens US-60-325-795-4
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                                                               Query Match
Best Local Similarity
Matches 97; Conserv
                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 610
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1698 TLGLE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1651 LQGQQVGVFAGTNGPHYEPL-------LRNTAEDLEGYVGTGNAASIMSGRVSY 1697
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116 LPLDLLLELNP----DAFSGPQACTRFFSRITKA----NVDLLPRGAPE-RQRLLPÅALA 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   114 DALPLDLLLFLNPDAFSGPQACTRFFSRITKANVDLLPR-----GAPERQRLLPAALA 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         596 DLSVQETLSGTPCLLGPGPVLTVLALLLASTLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EPVAIVGMACRLPGGVASPEDLWRLVAGGEDAISGFPQDRGWDV--EGLYDPDPDASGRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SRELGALTGAEQQRRMQELVREHLAVVLNHPSPEAVDTGRAFRDLGFDSLTAVELRNRLK 1491
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGGPPYGPPST---WSV-----STMDALR--GLLPVLGQPIIRSIPQGIVAAWRQR 272
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                                                                      Conservative 47; Mismatches 152; Indels 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                              3.0%; Score 99; DB 6; Length 24.9%; Pred. No. 1.2;
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GENERAL INFORMATION:
APPLICANT: Furness, Michael
APPLICANT: Buchbinder, Jenny
TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
FILE REFERENCE: PA-0041 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PERL Program SEQ ID NO 449 LENGTH: 308
                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/976,594
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 60/240,409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122 LRELPQEALDGLGSLRRLELEGNALEELRPGTFGALGALATLNLAHNALVYL--PAMAF- 178
                                                                                                                                    100
                                                                                                                                                                          137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    358 LQVPGAALRALPSLFSLHLQDNAVDRLAPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      238 GHNPLTYAGEEDGLALPGLRELLLDGGALQALGPRAFAHCPRLHTLDLRGNQLDTLPPLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          310 DESLIFYKKWE-----LEACVDAALLATOMDRVNAIPFTYEQLDVLKHKLDELYP-Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               167
                  228 GGPPYGPPSTWSVSTMDALRGLLPVLGQPIIRSIPQGIVAAWRQRSSRDPSWRQPERTIL 287
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                                                                                                                                                                                                                                                                                                                              19 LLFLLFSLGWVHPARTLAGETGTESAPLGGVLTTPHNISSLSPRQLLGFPCAEVSGLSTE 78
                                                                                                                                                                      RFFSRITKANVDLLPRGAPERQ------RLLPAALACWGVRGSLLSEADVRALGGLACD 189
                                                                                                                                                                                                            DSRFRELRKRYEDLLTRLRANQ-----SWEDSNTDLVPAPAVRILTPEVRLGSGG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GPGQLHLQHCGIAELEAGALAGLGRLIYLYLSDNQLAGLSAAALEGAPRLGYLYLERNRF
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                                                      ----ARPQAPALHLRL--SPPPSQSDQLLAESSSARPQLELHLRPQAARGRRRARARNG 200
                                                                                            LPGRFVAESAEVLLPRLVSCPGPLDQDQ-----
                                                                                                                                  HLHLRISRA---ALPEGLPEASRLHRALFRLSPTASRSWDVTRPLRRQLSL-----
                                                                                                                                                                                                                                                --RVRELAVALAQKNVKLSTEQLRCLAHRLSEPPEDLDALPLDLLLFLNPDAFSGPQACT 136
                                                                                                                                                                                                                                                                                        MLLVLLVLSWL------PHGGAL-----SLAEASRASFP--GPSELHTE 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -QGLLRVRWLRLSHNALSVLAPEALAGLPALRRLSLHHNELQALPGPVLSQARGLARLEL
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                                                                                                                                                                                                                                                                                                                                                                                       Score 96.5; DB 5; Pred. No. 0.69;
                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                       Length 308
                                                                                              -QEAARA----ALQG 227
                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                  147
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                                                                                        RESULT 14
US-09-897-516-6629
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CURRENT FILING DATE: 2001-10-11
NUMBER OF SEQ ID NOS: 194
SOFTWARE: PERL Program
SEQ ID NO 188
LENGTH: 308
TYPE: PRT
                                                      Sequence 6629, Application US/09897516 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Lasek, Amy W
APPLICANT: Jones, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 188, Application US/09981353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
            APPLICANT: Corbin, David R. APPLICANT: Goldman, Barry S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: GENES | FILE REFERENCE: PA-0038 US
  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE: Misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Incyte ID No: 522433CD1
                                                                                                                                                                                                      341 PFTYEQLDVLKHKLD 355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   201 DHCPLGPGRCCRLHTVRA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100 HLHLRISRA----ALPEGLPEASRLHRALFRLSPTASRSWDVTRPLRRQLSL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14 MLLVLLVLSWL--------PHGGAL-----SLAEASRASFP--GPSELHTE 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19 LIFLIFSLGWVHPARTLAGETGTESAPLGGVLTTPHNISSLSPRQLLGFPCAEVSGLSTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RFFSRITKANVDLLPRGAPERQ------KLLPAALACWGVRGSLLSEADVRALGGLACD 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SP---REVOVTMCIGACPSQFRAA-
                                                                                                                                                                    PASYNPM-VLIQKTD 289
                                                                                                                                                                                                                                                                                        RPRFRREVEKT----ACPSGKKAREIDESLIFYKKWELEACVDAALLATQMDRVNA---I 340
                                                                                                                                                                                                                                                                                                                              DHCPLGPGRCCRLHTVRA-----
                                                                                                                                                                                                                                                                                                                                                                  GGPPYGPPSTWSVSTMDALRGLLPVLGQPIIRSIPQGIVAAWRQRSSRDPSWRQPERTIL
                                                                                                                                                                                                                                                                                                                                                                                                                                             LPGRFVAESAEVLLPRLVSCPGPLDQDQ------QEAARA-----ALQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DSRFRELRKRYEDLLTRLRANQ------SWEDSNTDLVPAPAVRILTPEVRLGSGG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --RVRELAVALAQKNVKLSTEQLRCLAHRLSEPPEDLDALPLDLLLFLNPDAFSGPQACT 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RPRFRREVEKT----ACPSGKKAREIDESLIFYKKWELEACVDAALLATQMDRVNA---I 340
                                                                                                                                                                                                                                                SP---REVQVTMCIGACPSQFRAA----
                                                                                                                                                                                                                                                                                                                                                                                                           ----ARPQAPALHLRL--SPPPSQSDQLLAESSSARPQLELHLRPQAARGRRRARARNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jones, David A.
Hinkle, Gregory J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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Pred. No. 0.
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                                                                                                                                                                                                                                                -NMHAQIKTSLHRLKPDTVPAPCCV
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                                                                                                                                                                                                                                                                                                                              -SLEDLGWAD---WVL
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; NUMBER OF SEQ ID NOS: 8409
; SEQ ID NO 6629
; LENGTH: 689
; TYPE: PRT
; ORGANISM: Xenorhabdus sp.
US-09-897-516-6629
                                                                                                                                                                                                                                                                                                                                                             US-09-815-242-5107; Sequence 5107; A
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                 TITLE OF INVENTION: Identification of Essential TITLE OF INVENTION: Prokaryotes FILE REFERENCE: ELITRA.011A CURRENT APPLICATION NUMBER: US/09/815,242 CURRENT FILLING DATE: 2001-03-21 PRIOR APPLICATION NUMBER: 60/191,078 PRIOR FILING DATE: 2000-03-21
                                                                                                                                                                                                                                                         APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Spiridonov, Sergei
TITLE OF INVENTION: Xenorhabdus sp. Genome Sequences and Uses Thereof
FILE REFERENCE: 38-21(51847)B
CURRENT APPLICATION NUMBER: US/09/897,516
CURRENT FILING DATE: 2001-06-29
                                                                                                                                                                                                                      APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 205 LFRMVQQKTRAKTHGHYPAPERIIDVIRLGLEKGQK---AGL------QAEAKAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           135 CTRFFSRITKAN---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              148 GRQLKAKQAKRLGVVD---DAVPLDILLDVAVQYVKKGVAKRKPLAWSQRLLASSFGRPL 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88
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APPLICATION NUMBER: 60/
FILING DATE: 2000-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGLACD-----LPGRFVA-----ESAEVLLPRLVSCPGPLDQDQQEAARAALQGGGPPY 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SLPI------HQIAEIAKR--PEQVI 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LL---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----IANVTATRGHLPARIKDINEKGINQALKYTWDMLSKRVSQRRLTPSERSRQMS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91;
                                                                                                                                                                              Xu, H. Howard
                                                                                                                                                                                                                    Trawick, John D. Carr, Grant J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Malvar, Thomas M. Slater, Steven C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Huesing, Joseph E.
Krasomil-Osterfeld,
                                                                                                                                                                                                   Yamamoto, Robert T.
                                                                                                                                                                                                                                                                                                                                                               Application US/09815242
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                60/206,848
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US-09-815-242-5107
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Best Local Similarity 22.2
Matches 89; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ for Windows Version SEQ ID NO 5107
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PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        274 SRDPS-----WRQP---ERTILRPRF-----RREVEKTACPSGKKAREID 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     214 DQDQQEAARAALQGGGPPYGPPSTWSVSTMDALRGLLPVLGQPIIRSIPQGIVAAWRQRS
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                                                                                                                                                               DGVPVQRVHGDGGLHMDWQD-----FSALDRDSRQQHLQTLADSE--AHRPFDLES----
                                                                                                                                                                                                      ATLIDRFVKGRGQLDKDTLDTLTAFYPGYLCSLSPEELSSVPPSSIWAVRPQDLDTCDPR 477
                                                                                                                                                                                                                                                 W-QLEPDSPAYNVGGLARLSGPLDVARFEA----ALQALVQ---RHE----TLRTTFPSV
                                                                                                                                                                                                                                                                                        YPQGYPESVIQHLGYLFLKMSPEDIRKWNVTSLETLKALLEVDKGHEMSPQAPRRPLPQV 417
                                                                                                                                                                                                                                                                                                                                 LPLRALFEASELEAFCEQVRAAQAAGRTDSHGAIRRIDREQPVPLSYSQ-----QRMWFL
                                                                                                                                                                                                                                                                                                                                                                                                                 HVEPRTELQRRIAAIWSEVLGLPRVGLRDDFFELGGHSLLATRIVSRT-----RQACDVE 1686
FLDDRESPLEPLPVQYLDYSVWQR-EWLESGERQRQLDYW 1922
                                    FMKLRTDAVLPLTVAEVQKLLGPHVEGLKAEERHRPVRDW 568
                                                                                  ----GPLLRVCMVKMAEREHYLVV---
                                                                                                                                                                                                                                                                                                                                                                        ESL-IFYKKWELEA-C--VDAALLA-----TQMDRVNAIPFTYEQLDVLKHKLDEL
                                                                                                                      QLDVLYPKARLAFQNMNGSEYFVKIQSFLGGAPTEDLKALSQQNVSMDL-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 95.5;
Pred. No. 42;
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                                                                               -TLHHIVTEGWAMDIFARELGALYEA 1883
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Search completed: December 7, 2001, 09:49:36
Job time: 94 sec

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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Match
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Gapop 10.0 , Gapext 0.5
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3261
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Copyright (c) 1993 - 2000 Comp
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 В
E75503

835251

A835250

T13250

F75484

A41090

E83031

D82654

T08619

T49648

S75053
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T31352
B84683
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1448.747 Million cell updates/sec
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                                                                                      exodeoxyribonuclea
 hypothetical prote
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A; Molecule type: mRNA
A; Residues; 1-625 < YAM>
A; Residues; 1-625 < YAM>
C; Cross-references: DDBJ:D87351
C; Comment: This protein, as a tum
C; Genetics:
A; Gene: Erc

tumor marker for renal cell carcinoma,

is involved

'n

A; Map position: 10q12

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30
101	101	101.5	101.5	102	102	102.5	102.5	102.5	102.5	103.5	103.5	103.5	104	104	104
3.1	3.1	3.1	3.1	3.1	3.1	3.1	3.1	3.1	3.1	3.2	3.2	3.2	3.2	3.2	3.2
1997	677	2472	836	1160	1159	1239	1010	733	436	4128	1402	637	7576	1003	503
N	2	2	N	2		N	N	N	2	N	2	N	N	N	2
T30874	G02540	E83594	T30312	S34809	н64089	G71266	T36383	H69411	T28066	JC6306	S75938	A75342	T17428	B71469	A83027
virginiamycin S sy	nucleobindin - hum	still frameshift p	pilin biosynthetic	avrBs3-2 protein -	DNA-directed DNA p	probable ATP-depen	probable large ATP	cell division cont	hypothetical prote	protein kinase (EC	chemotaxis protein	hypothetical prote	FK506 polyketide s	glycinetRNA liga	hypothetical prote

ALIGNMENTS

Erc protein - rat
()Species: Rattus norvegicus (Norway rat)
()Species: Rattus norvegicus (Norway rat)
()C;Date: 17-Nov-2000 #sequence_revision 17-Nov-2000 #text_change 31-Dec-2000
()Accession: JC7362
R;Yamashita, Y.; Yokoyama, M.; Kobayashi, E.; Takai, S.; Hino, O.
Biochem. Biophys. Res. Commun. 275, 134-140, 2000
A;Title: Mapping and determination of the cDNA sequence of the Erc gene pre.
A;Reference number: JC7362
A;Accession: JC7362

gene preferentiall

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A;Residues: 1-2109 <DOW>
A;Cross-references: EMBL:M83200; NID:g468913; PID:g468914; PIDN:AAA73173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Title: Structure and evolution of the largest chloroplast A;Reference number: Z21012; MUID:94363755 A;Accession: T31352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Accession: T31352
R;Downie, S.R.; Katz-Downie, D.S.; Wolfe, K.H.;
Curr. Genet. 25, 367-378, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein - Pelargonium x hortorum
c;Species: Pelargonium x hortorum
C;Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 02-Sep-2000
C;Accession: T31352
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Best Local Similarity
Matches 128; Conserv
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- - PTREDDEIEDQAEMDTRRDLDGIEYTHAIQDMI-----
                                                                      PLITLEMEARSSWPFFQHLDEIYGDQLEYVYDDTSLSVEVEE----EEDTSWGIEEWSLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCDPRQLDVLYPKARL-AFQNMNGSEYFVKIQSFLGGAPTEDLKALSQQNVSMDLATFMK
                                                                                                                                                   YQTMTYSKTSCGVNAFHFPSHEKPFSFRLDLSPPRGILVIGSIGTGRSYLIKSLAKNTHF
                                                                                                                                                                                                                         VDQILLSLTQSSKNASGSQMIEQPGEMYLR-HVVDLQKKYLMGYEFNTSSLAERRIFLAH 1299
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                                                                                                                                                                                                                                                                                                                                     EKTACPSGKKAREIDESLIFYKKW----ELEACVDAALLATQMDRVNAIPF-----TYEQ
                                                                                                                                                                                                                                                                                                                                                                                 SNWNLNLID-ISDLISLIPNPIDR-ITFSINTRHLSHTSKE----IYSFIRKRER---
                                                                                                                                                                                                                                                                                                                                                                                                      STWSVSTMDALRGLLPVLGQPIIRSIPQGIVAAWRQRSSRDPSWRQPERTILRPRFRREV 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DVRALGGLACDLPGRFVAESAEVLLPRLVSCPGPLDQDQQEAARAALQGGGPPYGPP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACTRFFSRITKANVDL-----LPRGAPERQRLL----PAALACWGVRGSLLSEA 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RIREIS-RMCLRNLTLSAERIRRNNESPLTHTHLRSPNVLEFLYSTLLLLL----VAGYL 1060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RVRELAVALAQKNVKLSTEQLR-----CLAHRLSEPPEDLDALPLDLLLFLNPDAFSGPQ 133
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                                                                                                                                                                                        -----VDKGHEMSPQAP---RRPL--PQVATLIDRFVKGRGQLDKD-----
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20.5%; Pred. No. 2.2;
Live 91; Mismatches
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                                                                                                               -DTLTAFYPGYLCSLSPEELSSVPPSSIWAVRPQDLD
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A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-2218 <STO>
A;Cross-references: GB:AE002093; NID:g4803953; PIDN:AAD29825.1; GSPDB:GN00139
C;Genetics:
C;Gene: At2g28300
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A;Title: Sequence and analysis of chromosome
A;Reference number: A84420; MUID:20083487
A;Accession: B84683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P. M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein At2g28300 [imported] - Arabidopsis thaliana c;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001 C;Accession: B84683
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                                            HEMSPQAPRRPLPQVATL-
                                                                                        VGE--PSATTRTNVPD-----AQSPGEM---NLHTVETHKAEDSSGLKNQEALYNLSKA
                                                                                                                                LDELYPOGYPESVIQHLGYLFLKMSPEDIRKWNVTSLETLK-----ALLEVDKG
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DKLVSDIP-HPVPGDLTTSGSVANKDVDIGSSKVAAENELVKIPGGDVDSSVIQLSLGNT
                                                                                                                                                                                                                                                                                                                  SSRDPSWRQPER------RPRFRR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LAVALAQKNVKLS--TEQLRCLAHRLSEPPEDLDALPLDLLLFLNPDAFSGPQACTRFFS 140
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                                                                                                                                                                             SVAPDIHSSGSLSQEIRRDTSGTGGSARKQTADVTDVARVMKEI-----FSETSLLKHK
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VKGRGQLDKDTLDTL----

TAFYPGYLCSLSPEELSSV---

-PPSSIWAVR 467

	460 1 4048	Qy 419TLIDREVKGRQQLDKDTLDTLTAFYPGYLCSLSPEELSSVPP	Ωу
	1 418 1 3988	Qy 371 GYLFLKMSPEDIRKWNVTSLETLKALLEVDKGHEMSPQAPRRPLPQVA	Оγ
	370 A 3933	Qy 312 SLIFYKKWELEACVDAALLATOMD-RVNAIPFTYBOLDVLKHKLDELYPOGYPESVIOHL	Оу
	311	Qy 265 IVAAWRORSSRDPSWRQPERTILRPRFRREVEKTACPSGKKARĖIDE ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ;	do Vy
	3 264 1 3830	Qy 210 PGPLDQDQQEAARAALQGGGPPYGPPSTWSVSTMDALRGLLPVLGQPIIRSIPQG	g 9
	3774	Qy 172 GSLLSEADVRALGGLACDLPGRFVAESAEVLL	DP QA
	3722	Qy 114 DALPLDLLLFLNPDAFSGPQACTRFFSRITKANVDLLPRGAPERQRLLPAALACWGVR	Db Og
	113	Qy 66 GFPCAEVSGLSTERVRELAVALAQKNVKLSTEQLRCLAHRLSEPPEDL :: :: :: :: 3615 GQLRAQLQGVLAKNPQLRHLSPQQQQQLQALLMQRQLQQSQAVRQTPPYQEPGT	g dy
	3614	Qy 8 PCWSCGDRPGSLLFLLFSLGWVHPARTLAGETGTESAPLGGVLTTPHNISSLSPRQLL	Оy
	Gaps 34;	Query Match 3.4%; Score 111.5; DB 2; Length 4957; Best Local Similarity 19.9%; Pred. No. 74; Matches 148; Conservative 112; Mismatches 287; Indels 195;	X E O
	PID: g2358287	e type: mRNA s: 1-4957 <pra> eferences: EMBL:AF010404; NID:g2358286; PIDN:AAC51735.1; S: LR ition: 12 mily: human ALR protein s: alternative splicing</pra>	X X X Q Q C X X I
	gene with strong homolog	expression pattern of human ALR, a novel 1954; MUID:97388474 translated from CR/FWRT/DDBT	A A ; A
	Jul-2000 Rallapalli, R.; Yano,	ein - human s: Homo sapiens (man) 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 21- ion: T33455 , R.; Zhadanov, A.B.; Sedkov, Y.; Bullrich, F.; Druck, T.; 15, 549-560, 1997	On C; S; D; D; S; D; D; S; D;
			RES TO3
		Qy 524 MDLATFMKLRTDAVLPLTVAEVQKLLGPHVEGLKAEERHRPVRD 567	Фф
	741	Oy 468 PODLDTCDPROLDVLYPKARLAFONMNGSEYFVKIOSFLGGAPTEDLKALSOONVS : ; : : : : : :	Db Oy
_	697	Db 642 LTAKSSLEKCTADQLLGEKLSQEGETTPASDGETCHLAEETASSLSYVRSEPTASA	рь

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ALR protein - human (man) (;Species: Homo sapiens (man) (;Species: Homo sapiens (man) (;Species: Homo sapiens (man) (;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 21-Jul-2000 (;Accession: T03454 R;Prasad, R.; Zhadanov, A.B.; Sedkov, Y.; Bullrich, F.; Druck, T.; Rallapalli, R.; Ya Oncogene 15, 549-550, 1997 A;Title: Structure and expression pattern of human ALR, a novel gene with strong homo A;Reference number: Z14954; MUID:97388474 A;Accession: T03454
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C;Superfamily: human ALR protein
C;Keywords: alternative splicing
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C;Genetics:
A;Gene: ALR
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A; Residues: 1-5262 <PRA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3920 GQLRAQLQGVLAKNPQLRHLSPQQQQQLQALLMQRQLQQSQ-----AVRQTPPYQEPGT 3973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3862 PSVSLGDQPGSMTQNL--LGPQQPMLERPMQNNTGPQPPKPGPVLQSGQGLPGVGIMPTV 3919
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4049 TPPPSVQQKMVNGVTPSEELGEHPKDAASARDSERALRDTSE--VKSLDLLAALPTPPHN 4106
                                                           4190 KLLRAKNVQLSTGQGSEGLRAEINGHIDS-----KLAGLEQKL-----QGTPSNKEDAA 4238
                                                                                                                                                                                                                                                                                                                                                                                                                              4028 GPVHPTPPPSSPQEPKR-----PSQLPSPSSQLPTEAQLPPTHPGTPKPQGPTLEPP 4079
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3974 QTSPLQGLLGCQPQLGGFPGPQT-----GPLQELGAGPRPQG-PPRLPAPPGALSTGPVL 4027
                                                                                                                                                                                                                                                                                                    4080 PGRVSPAAAQLADTLFSKGLGPWDPPDNLAETQKPEQSSLVPGHLDQVNGQ-----VVPEA 4135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             461 SSIWAVRPQDLDTCDPRQLDVLYPKARLAFQN-----MNGSEYFVKIQSFLGGAP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    172 GSL-----LSEADVRALGGLACDLPGRFVAESAEVLL-------PRLVSC 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        114 DALPLDLLLELNPD -- AFSGPQACTRFFSRITKANVDLLPRGAPERQRLLPAALACWGVR 171
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371 GYLFLKMSPEDIRKWN---VTSLETLK-----
                                                                                                                                                                                                                                           265 IVAAWRQRSSRDPSWRQPERTILRPRFRREVE------KTACPSGKKAREIDE 311
                                                                                                                                                                                                                                                                                                                                                            210 PGPLDQDQQEAARAALQGGGPPYGPPSTWSVSTMDALRGLLP-----VLGQPIIRSIPQG 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66 GFPCAEVSG-----LSTERVRELAVALAQKNVKLSTEQLRCLAHRLSEPPED--L 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 PCWSCGDRPGSLLFLLFSLGWVHP--ARTLAGETGTESAPLGGVLTTPHNISSLSPRQLL
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                                                                                                             SLIFYKKWELEACVDAALLATOMD-RVNAIPFTYEOLDVLKHKLDELYPOGYPESVIOHL 370
                                                                                                                                                                                   SQLSIKQEPREEPC-----ALGAQSVKREANGEPIGAPGTSNHLLLAGPRSEAGHLLLQ 4189
-ALLEVDKGHEMSPQAPRRPLPQVA 418
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hypothetical protein F8A5.20 [imported] - Arabidopsis thaliana (C.Specles: Arabidopsis thaliana (mouse-ear cress) C.Specles: Arabidopsis thaliana (mouse-ear cress) C.Specles: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001 C.Accession: B9632 R.Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dew ansen, N.F.; Hughes, B.; Huizar, L. Nature 408, 816-820, 2000 A.; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Ma A.Authors: Salzberg, T.; Rowley, D.; Sakano, H. Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. Rizzo, M.; Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; T. ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A.; Feference number: A86141; MUID:21016719
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C;Superfamily: fission yeast pyridoxine 4-dehydrogenase
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A; Residues: 1-340 <STO>
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A; Accession: B96632
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Best Local
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PSWROPERT LRPRFRREVEKTACPSGKKAREIDESLIFYKK---
                                         RAHAVHPITAVQIEWSLWSRDAEEDIIPICRELGIGIVAYSPLGRGFLAAGPKLAENLEN
                                                                                                                       RAACEASLKRLDIACIDLYYQHRIDTRVPIEITMRELKKLVEEGKIKYIGLSEASASTIR
                                                                                                                                                          AESAEVLLPRL-VSCPG-----PLDQDQQEAARAALQGG----GPPYGPPST--
                                                                                                                                                                                                   ---DTSDMYGPETNELLLGKALKDGVKEKVELATKFGFFIVEGEISEVRG----DPEYV
                                                                                                                                                                                                                                          ANVDLLPRGAPERQRLLPAALACWGVR------GSLLSEADVRALGGLACDLPGRFV 195
                                                                                                                                                                                                                                                                                   LGSQGLEVSAQGLGCMALSARYGAPKPETDAIAL-----LHHAINSG----VTFF-----
                                                                                                                                                                                                                                                                                                                    LAQKNVKLSTEQLRCLA -- HRLSEPPEDLDALPLDLLLFLNPDAFSGPQACTRFFSRITK 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LNG-----VMVAVAELLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SSIWAVRPQDLDTCDPRQLDVLYPKARLAFQN-----MNGSEYFVKIQSFLGGAP-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ITANESLEAPEGSGCPVNGQSQLRGAEGSGALPTGPDYYSQLLTKNNLSNPPTPPSSLPP 4353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----TLIDRFVKG-
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89; Conserv
                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                -WSVSTMDALRGLLPV---LGQPIIRSIP--QGIVAAWRQ--RSSRD 276
                                                                                                                                                                                                                                                                                                                                                                                 3.4%;
                                                                                                                                                                                                                                                                                                                                                                 62;
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                                                                                                                                                                                                                                                                                                                                                                               Score 110.5;
Pred. No. 2;
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    -WELEACVDAALLAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-1770 <POS>
A; Cross-references: EMBL:U24657; NID:g1171127; PID:g1171128;
A; Experimental source: strain DM504-15
C; Genetics:
A; Gene: safB
C; Superfamily: acetate--CoA ligase homology; acyl carrier pro C; Keywords: carrier protein
F; 72-577/Domain: acetate--CoA ligase homology <ACL>
F; 618-688/Domain: acetate--CoA ligase homology <ACP1>
F; 1222-1659/Domain: acetate--CoA ligase homology <ACP2>
F; 1678-1746/Domain: acyl carrier protein homology <ACP2>
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A;Title: Two multifunctional peptide synthetases
A;Reference number: 218967; MUID:97090395
A;Accession: T18551
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  saframycin Mx1 synthetase B - Myxococcus xanthus
C;Species: Myxococcus xanthus
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999
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                                                                                                                                                                                                                                          EAAGREARPVSAPTPGTGERLPVPPGQRALW
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                                                                              VQQVHAHVPASFLVVDASGD-----DEAALRRRLLREA--
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Pred. No. 22;
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----QMDRVNAIPFTYEQLDVLKHKLDELYPQGYPESVIQHLGYLFLKMSPEDIRKWNVT 388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       - NVDHNKILFEKVSAMAEKKGCTPAQLALA
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PID:g1171128;
                                                                                                                            and an
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                                                                                                                               O-methyltransferase
PIDN: AAC44128
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580 AYLEGQLDTVSADAAQEPVGEFSLSRASLLERSEAERLPALVAYLASAATRAGSLPRAIL 520 VVVQEVDRRYPGGDWPDVIAAIRRDISEQHALRVHAVVLIKSGSLLKTSSGKVQRGATRE 44 APLGGVLTT-----PHNISSLSPRQLLGFPCAE----VSGLSTERVR--ELAVALA KKWEL-----EACVDAALLATQMDRVNAIPFTYEQLDVLKHKLDELYPQGYPE QKNVKLSTEQLRCLA-----HRLSEPPEDLD-ALPLDLLLFLNPDAFSGPQACTRFFSRI 142 RPFDLGRGPLLRTHLFSRAAQEHVLLLS-----VHHIVVDFWSLAVLVDELRRLYEAGGDG TKANVDLLPRGAP-----ERQRLLPAALACWGVRGSLLSEADVRALGGLACDLPGRFVAE TGEVRLPDLGLDSLALVELKHRIE----QDLEVALELRLLL------EGPTLGALAVHLL IRSIPQGIVAAWR-QRSSRDPSWRQPERTILRPRFRREVEKTACPSGKKAREIDESLIFY 316 SAEVLLPRLVSCPGPLDQDQQEAARAALQGGGPPYGPPSTWSVSTMDALRGLLPVLGQPI RAICLQGALD---VEALRRAFQS------LVTRHPALRATFPMVGEEP 175; 2: -----TLAGET---GTES 43 Length 1770; -FLHQLAPDSPGYTIA-Indels 142; Υ----Gaps 197 864 364 808 774 735 689 639 88 579 257 22;

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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues; 1-1171 <SEE>
A;Cross-references: EMBL:AL096825; PIDN:CAB46976.1; GSPDB:GN00070; SCOEDB:SC6G3.04
A;Cxperimental source: strain A3(2)
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C;Accession: T35548

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                                                                                                                                                                                                                                                                                                          817
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  959
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  642 ERRLTGVLVAAGFLIESASTALGPLFERVETMSDRGFLDRLYALRGGFRALTPQG---RS 698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       582 RLGLRLDGELYALSRRGSPLLQGAAQAARVLLDLDGSDLLGTRLAGWVDTATGPDGRRRL 641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            402 LQRLKECGVGYAEPVEVTGAGEGSALTTRWRAAWTPSVAARLDLVGVRGVTAAQAADGTL 461
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            217 QQEAARAALQG------GGPPYGPPSTWSVSTMDALRGLLPVLGQPIIRSIP-----QG 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                159 RLLPAALACWGVRGSLLSEADVRALGGLACDLPGRFVAESAEVLLPRLVSCPGPLD--QD 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      116 --- LPLD------PDAFSGPQACTRF 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      522 LDSVRRRHLPGTTETVRIRAARLAGLLLDAAVRLLPGLAGSDEPRDAVAVVTLAVRSAAD 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          462 RENHRRAAEAGRVTSARVVALLGAAARCALTDLLHDGLTEAERVLPGAAALPELLAALDL 521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51 TTPH-----NISSLSPRQLLGFP--CAEV----SGLS-TERVRELAVALAQ------
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                                                                                                                                                                                                                                                                                                        EEADEESRETNEGGDGGEPEPGAGGTSEGSDDDRTGGAARSFPSVRHWAEDLRTLFGAET 876
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RRPGGPLDLPRTLRANLAHIRRREDGRVEVVPERPVFRTRTARRNDWRLILVVDVSASME 1018
                                               RRP-----LPQV--ATL--IDRFVKGRGQL--DKDTLDTLTAFYPGYLCSLSPEELSSVP 459
                                                                                                    ----LTLARGMPEQRVASLRPL-VKRLVEELTKELATRLRPTLTGL--
                                                                                                                                                 HKLDELYPQGYPESVIQHLGYLFLKMSPEDIRKWNVTSLE-TLKALLEVDKGHEMSPQAP 410
                                                                                                                                                                                                      RQEVLERAVADGRT------DVIALLDPASVRPSVELLSAV------
                                                                                                                                                                                                                                                   RREVEKTACPSGKKAREIDESLIFYKKWELEACVDAALLATQMDRVNAIPFTYEQLDVLK 351
                                                                                                                                                                                                                                                                                                                                                          SAPAPRTAPSGAEVPHGAGAPRLGPADRWRLLLGRDTAG-LPAALRPYARALDELFDREG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RVLAAVSDRLGDRPDLRLPAPAELVGRWAA-ADGEGLALLGELGLADLASAPAAKDAGAT 757
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                                                                                                    -TTPRPT 958
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540LGHL	Db 432 ITPYGVLEMLENRKLADPSVLDDPKEALRLGYRFDSFRDRYQAMFDVLKQRLHIPQDKVE 491 Qy 305KAREIDESLIFYKKWELEACVDAALLATQMDRVNAIPFTYEQLDVLKHKLDELYP 359	147 VDLLPRGAPERQRLLPAALACW-GVRGSLLSEADVRALGGLACDLPGREVAESAEVLLPR	QY 22 LESSON PERKLENGELGES AFRICAGNELL FINE STATEMENT OF A CONTROL OF	Query Match 3.3%; Score 108.5; DB 2; Length 652; Best Local Similarity 22.6%; Pred. No. 6.8; Matches 98; Conservative 44; Mismatches 143; Indels 149; Ga	RESULT 9 G82962 G82962 C;Dacies: Pseudomonas aeruginosa C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000 C;Accession: G82962 R;Stover, C. K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L. JLOTY, S.; Olson, M.V. Nature 406, 959-964, 2000 A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa A;Reference number: A82950; MUID:20437337 A;Accession: G82962 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-652 <sto> A;Cross-references: GB:AE004959; GB:AE004091; NID:g9951791; PIDN:AAC08849.1; GSPDB:GN A;Experimental source: strain PAO1 C;Genetics: A;Gene: PA5464</sto>	Qy 460 PSSIMAVRPQDLDTCDPRQLDVLYPKARLAFQNMNGSEYFVKIQSFLGGAPT

C; Superfamily: probable DNA helicase MJ0104

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hypothetical helicase - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03 Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Nov-2000
C;Accession: T39568
R;Wood, V: Rajandream, M.A.; Barrell, B.G.; Brown, D.; Churcher, C.M.
submitted to the EMBL Data Library, March 1999
A;Reference number: Z21864
A;Accession: T39568
A;Atcus: preliminary; translated from GB/EMBL/DDBJ
A, Status: preliminary; translated from GB/EMBL/DDBJ
A; Map position: 2
A; Introns: 120/1;
                                                                              A;Cross-references: EMBL:AL035637; PIDN:CAB38508.1; A;Experimental source: strain 972h-; cosmid c16D10 C;Genetics:
                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-1398 < WOO>
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A;Introns: 120/1; 1051/2; 1289/3
C;Superfamily: probable DNA helicase MJ0104
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A;Accession: T51292
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Kang, H.Y.; Choi, E.; Lee, K.H.; Bae, S.H.; Gim, B.S.; Park, C.; MacNeill, S.A.; submitted to the EMBL Data Library, April 1999
A;Description: Genetic characterization of dna2+, a schizosaccharomyces pombe homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Schizosaccharomyces pombe
C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 17-Nov-2000
C;Accession: T51292
                                                         A; Gene: SPDB:SPBC16D10.04c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-1397 <KAN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Cross-references: EMBL: AF144384;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIFNKRKEDYCIIDEASQIPL---PICLGP 1078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GIPN----GYLVLDLSVQETLSGTPCLLGP 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GIASIRGTL-----MSSVLPDAPLIIRDMIIRLKPPKFCNSALIDPEFLKCLNEDQIT 938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LTAFYPGYLCSLSPEELSSVPPSSIWAVR------PQDLDTC--DPRQLDVLYPKARL 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLEIDDRVFHYKFAFLNDNGYPRNFL-HSGFSVGERVFIS---DEHGHWSLAKGHIVHIQ 827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REVKDEDLEFYKKWEKLLNQEERLLL--LKRGDVLTFDTEELEAYGKTLYPLYITKEDIV 771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REI-DESLIFYKKWELEACVDAALLATQMDRVNAIPFTYEQLD-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DSTIVRLGSPH-----KIHPLVKEFCLTEGTTFDDLASLKHFYEDPQIVACSSLGVYH 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -AEVQKLLGPHVEGLKAEERHRPVRDWILRQRQ--DDLDTL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AFQNMNGSEYFVKIQSFLGGAPTEDLKALSQQNVSMD----LATFMKLRTDAVLPLTV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DSCIEVRTRHRL--HIPWLKMPNFDFKKNQVFFGNYEDSKLSFIGSNHTRYRIDKDEFSS 885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KALLEVDKGHEMSPQAPRRPLPQVATLIDRFVKG-------RGQLDKDTLDT 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALKKCHAAEHYSLILGMPGTGKTTTISSLIRSLLAKKKKILLTSFTHLAVDNILIKLKGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----VLKHKLDELYPQGYPESVIQHLGY-----LFLKMSPEDIRKWNVTS---LETL 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
             1052/2; 1290/3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 108.5;
Pred. No. 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIDN; AAD38528
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                                                                                                                        GSPDB:GN00067; SPDB:SPBC16D10.04c
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Best Local
1053 SIFNKRKFDYCIIDEASQIPL---PICLGP 1079
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                                587 GIPN----GYLVLDLSVQETLSGTPCLLGP 612
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                                                                                                                                                                                                                                                                                                                                                                   773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
les 83; Conserv
                                                                                                                                                                                                                                                                                                                            KALLEVDKGHEMSPQAPRRPLPQVATLIDRFVKG-------RGQLDKDTLDT 438
                                                                     DSTIVRLGSPH-----KIHPLVKEFCLTEGTTFDDLASLKHFYEDPQIVACSSLGVYH 105:
                                                                                                                                            ALKKCHAAEHYSLILGMPGTGKTTTISSLIRSLLAKKKKILLTSFTHLAVDNILIKLKGC
                                                                                                                                                                                                               GIASIRGTL-----MSSVLPDAPLIIRDMIIRLKPPKFCNSALIDPEFLKCLNEDQIT 939
                                                                                                                                                                                                                                                   LTAFYPGYLCSLSPEELSSVPPSSIWAVR------PQDLDTC--DPRQLDVLYPKARL 488
                                                                                                                                                                                                                                                                                          DSCIEVRTRHRL--HIPWLKMPNFDFKKNQVFFGNYEDSKLSFIGSNHTRYRIDKDEFSS
                                                                                                                                                                                                                                                                                                                                                                                                   -----VLKHKLDELYPQGYPESVIQHLGY-----LFLKMSPEDIRKWNVTS---LETL 393
                                                                                                                                                                                                                                                                                                                                                                                                                                      REVKDEDLEFYKKWEKILNQEERLLL--LKRGDVLTFDTEELEAYGKTLYPLYITKEDIV 772
                                                                                                         -AEVQKLLGPHVEGLKAEERHRPVRDWILRQRQ--DDLDTL------GLGLQG
                                                                                                                                                                            AFQNMNGSEYFVKIQSFLGGAPTEDLKALSQQNVSMD----LATFMKLRTDAVLPLTV--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 108.5;
Pred. No. 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:U70852; PIDN:AAB09135.1; GSPDB:GN00022; CESP:F45E4.4 A;Experimental source: strain Bristol N2; clone F45E4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein F45E4.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T25752
                                                                                                                                                                                                                                                                                                                                                                                                                    A; Map position: 4
A; Introns: 60/2; 111/2; 939/3; 977/2; 998/1; 1021/1; 1125/3; 1140/3; 1157/2; 1173/2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Gene: CESP:F45E4.4
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A; Residues: 1-2361 <WIL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Description: The sequence A;Reference number: 220082 A;Accession: T25752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        submitted to the EMBL Data Library, September 1996 A; Description: The sequence of C. elegans cosmid F45E4
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                                                                                                                                                                                                                                                                                                                                               Query Match
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     1215
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                                                  103
                                                                                                                                                   58
                                                                                                                                                                                                                                               16 PGSLLFLLFSLGWV----HPARTLAGETGTE---SAPL------GGVLTTPHNIS
                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                 SLS-----PRQLLGFPCAEVSGLSTERVRELAVALAQ-----KNVKLSTEQLRCL 102
                                                                                                                                                                                                                                                                                               134;
SSNIPAGMEDLSEAEREKIMSVMANAEMEMGARFPPPSSQIPTRSPSVMSSSIMSELPPG
                                                  AHRLSEPPEDLDALPLDLLLFLNPDA-----FSGP--QACTRFFSRITKANVDLLPRG 153
                                                                                                   SLGTSAPTKSIPSPQIGIP---MDGLSEEERRQIMSVMAAADFDDSVNNVKPSTSG----
                                                                                                                                                                                                                                                                                                  Conservative 114; Mismatches
                                                                                                                                                                                                                                                                                                                        3.3%; Score 108.5;
19.4%; Pred. No. 43;
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     1274
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Length

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A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A;Reference number: A82515; MUID:20365717

A;Note: for a complete list of authors see reference number A59328 below

A;Accession: B82662

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-283 <SIM>
A;Pesidues: 1-283 <SIM
A;Pesidues: 1-
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C; Date: 18-Aug-2000
C; Accession: E82662
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R; anonymous, The ...

151-157,
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                                                     A;Contents: annotation C;Genetics: A;Gene: XF1602
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                                                                                                                                               A; Reference number: A59328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QKLLGPHVEGLKAEERHRPVRDWILRQRQDD 576
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5-oxoprolinase (ATP-hydrolyzing) (EC 3.5.2.9) - rat
N,Alternate names: pyroglutamase (ATP-hydrolyzing)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 11-May-2000
C:Accession: T42756
R:Ye, G.J.; Breslow, E.; Melster, A.
J. Biol. Chem. 271, 32293-32300, 1996
A;Title: The amino acid sequence of rat kidney 5-oxo-L-prolinase determined A;Accession: T42756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1288 <YEG>
A;Cross-references: EMBL:U70825; NID:g1732064; PID:g1732065; PIDN:AAC52955.1
A;Experimental source: strain Sprague-Dawley; Kidney
C;Superfamily: hypothetical protein YKL215c
C;Keywords: homodimer; hydrolase
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                                                                                                                                                                                                                                                                                                                                                                                                                           265 VLFMR-SDGGLAPMDAFSGSRAVLSGPAGGVVGYSATTYHLEGGQP--VIGF---DMGGT 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              258 QLAPLGTTSTPSLADLFV
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                                                 ----GPPSTWSVSTMDALRGLLPVLGQPIIRSIPQGIVAAWRQRSSRDPSWRQPERTILR 288
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FLTNGPCPASQLSLEEVAMGFVRVANEAMCRPI - - - - RALTQARGHDPS - - -
                                                                                                                                                                                                                                          -DLLLFLNPD---AFSGPQACTRFFSRITKANVDLLPRGAPERQRLLPAALACWGVRGSL
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                                                                                                                                                          LSEADVRALGGLACDLPGREVAESAEVILLPRLVSCPGPLDQDQQEAARAALQGGGPPY--
                                                                                                                                                                                                               RSGLFVVGPESAGAHPGP-ACYRKGGPVTVTDANLV-----LGRLLPASFPC-----
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Pred. No. 2.
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Pred. No. 21;
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A;Description: catalyzes the construction of a polyketide chain, which is then cyclised A;Pathway: erythromycin biosynthesis C;Superfamily: [acyl-carrier-protein] S-malonyltransferase homology; 3-oxoacyl-[acyl-carrier-thain alcohol dehydrogenase homology construction alcohol dehydrogenase homology construction; coenzyme A; multic;Keywords: acyltransferase; antibiotic biosynthesis; carrier protein; coenzyme A; multic;S2-453/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology coAs1> F;561-843/Domain: [acyl-carrier-protein] S-malonyltransferase homology cAMT1>
                                                                                                                                                                                                                                                                                                          A; Title: Identification of DEBS 1, DEBS 2
A; Reference number: S23103; MUID:92316235
A; Accession: S23205
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                                                                                                                                                                 C; Function:
                                                                                                                                                                                      A;Gene: eryA
A;Start codon: GTG
                                                                                                                                                                                                                                                                              A; Molecule type: protein A; Residues: 2-12, 'XXX' <
                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:X62569; NID:g46977; PIDN:CAA44448.1; PID:g58165:R;Caffrey, P.; Bevitt, D.J.; Staunton, J.; Leadlay, P.F.
FEBS Lett. 304, 225-228, 1992
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A; Reference number: S23070; MUID:
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C;Accession: S23070; S22011; S23205
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                                                                                                                                                                                                                                                         A;Experimental source: strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             submitted to the EMBL Data Library, A; Reference number: S22011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Experimental source: strain R;Bevitt, D.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: DNA
A:Residues: 1-3573 <BEV1>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: S23070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   \;Molecule type: DNA
\;Residues: 1-184,'I
                                                                                                                                                                                                                                                                                                                                                                                                                                                            479, 'DH', 3480-3572 <BEV2>
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561-843/Domain:
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F;1519-1919/Domain: 3-oxoacyl-[acyl-carrier-protein] Synthase I homology
F;2023-2305/Domain: lacyl-carrier-protein] S-malonyltransferase homology
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                                  -GLQGGIPNGYLVLDLS--VQETLSGTPCLLGPGPVLTVLAL 621
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2000 Compugen
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Q13421;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chang K., Pastan I.; "Molecular cloning of mesothelin, a differentiation antigen present on mesothelium, mesotheliumas, and ovarian cancers."; proc. Natl. Acad. Sci. U.S.A. 93:136-140(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
MESOTHELIN PRECURSOR (CAK1 ANTIGEN).
                                                                                                                                                                                                           use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                            Int. J. Cancer 57:90-97(1994).
-!- FUNCTION: MAY PLAY A ROLE IN CELLULAR ADHESION. ANTIGENIC PROTEIN
REACTIVE WITH ANTIBODY K1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Carcinoma;
MEDLINE=96133892; PubMed=8552591;
   CARBOHYD
                                                                                                                                                           EMBL; U40434; AAC50348.1; MIM; 601051; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               detected by the K1 antibody from an ovarian carcinoma (OVCAR-3) cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND CHARACTERIZATION MEDLINE=94200897; PubMed=8150545;
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TISSUE SPECIFICITY: EXPRESSED IN MESOTHELIAL CELLS, MESOTHELION OVARIAN CANCERS, AND SOME SQUAMOUS CELL CARCINOMAS.
PTM: GLYCOSYLATED.
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Y076_HUMAN
TEGU_HCMVA
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NDI1_YEAST
RYNR_PIG
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GPPA_ECOLI
PKL2_HUMAN
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CYGD_CANFA

CYGE_RAT
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MPI2_RAT

CYGD_HUMAN

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SPK_HUMAN
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DP3A_HAEIN
LGN_HUMAN
RAG1_ONCMY
NCB1_HUMAN
ITB4_RAT
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US-09-215-035-2 3261

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December 7, 2001, 09:47:57

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Maximum Match 100% Listing first 45 summaries

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MEDLINE-98088960; Pubmed-9428684;

Pallga K., Peraus G., Kreger S., Duwrrwang U., Hesse L

Masters C.L., Beyreuther K., Weldemann A.;

"Human amyloid precursor-like protein 1--cDNA cloning,
expression in COS-7 cells and identification of soluble
                                                                                                                                                                                                                                                                                             APPL_HUMAN STANDARD; PRT; 650 AA.
APPL_HUMAN STANDARD; PRT; 650 AA.
P51693; 000113;
01-OCT-1996 (Rel. 34, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
AMYLOID-LIKE PROTEIN 1 PRECURSOR (APLP).
                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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Best Local Similarity 19.1%;
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lenkkeri U., Kestila M., Lamerdin J., McCready P., Olsen A., Tryggvason K.;
"Structure of the human amyloid-precursor-like prot 19913.1.";
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SIGNAL
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Eur. J. Biochem. 250:3
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TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN BRAIN, PARTIC IN THE CEREBRAL CORTEX POSTSYNAPTIC DENSITY.

PTM: N- AND O-GLYCOSYLATED.

SIMILARITY: BETOMOG T-
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PSTRSWPPGSRVEGAEDEEEEESFPQPVDDYFVEPPQAEEEEETVPPPSSHTLAV----
                                                  AQEACSSQGLILHGSGMLLPCGSDRFRGVEYVCCPPPGTPDPSGTA------
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                                                                                                                                                                                                                                                                                                                       MW;
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Pred. No. 0.37;
79; Mismatches 2
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POTENTIAL.
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"-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

P -> A (IN REF. 2).

121A034B708C67CA CRC64;
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CLATHRIN-BINDING (POTENTIAL).
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GUCYZE OR GUCAL
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Mus musculus (Mouse).
Metazoa; Chordata;
Metazoa; Rodentia;
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                       HSSP;
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                                                                                                                                                                          s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
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InterPro; IPR001054; Guanylt_cyclase.
Pfam; PF010194; ANF_receptor; 1.
Pfam; PF00211; guanylate_cyc; 1.
Pfam; PF00069; pkinase; 1.
SMART; SM00044; CYCC; 1.
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                                                                                                                                WLKKFPGEHHMAIRPATKTAFSKLRELRHENVALYLGLFLAGTADSP--ATPGEGILAVV
                                                                                                                                                             LRPRERREVEKTACPSGK----KAREI-DESLIFYKKWELEACVDAALLATQMDRVNAI-
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                                                                 SEHCARGSLHDLLAQREIKLDWMFKSSLLLDLIKGMRYLHHRGVAHGRLKSRNCVVDGRF
                                                                                                                                                                                                IILTLEDVTFLHPPGGSSRKVVQGSRSSLATRSASDIRSVPS--QPQESTNVGLYEGDWV
                                                                                                                                                                                                                                                                 PGPDPSCWFDPDVICNGGVEPGLVFVGFLLVIGMGLTGAFLAHYLRHRLLHMQMASGPNK
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GUANYLYL CYCLASE GC-E.
EXTRACELLULAR (POTENTIAL)
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
PROTEIN KINASE-LIKE.
GUANYLATE CYCLASE.
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INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
N-LINKED (GLCNAC...) (POTENTIAL).
MW; A1CC9E1B1444C803 GRC64;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-21201183; PubMed-11278896; Fujiwara S., Takeo N., Otani Y., Parry D.A.D., Kunimatsu M., Lu R., Sasaki M., Matsuo N., Khaleduzzaman M., Yoshioka H.; Sasaki M., Matsuo N., Khaleduzzaman M., Yoshioka H.; "Epiplakin, a novel member of the plakin family originally identified as a 450-kDa human epidermal autoantigen: structure and tissue localization.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
EPIPLAKIN (450 KDA EPIDERMAL ANTIGEN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Cervical carcinoma;
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TISSUE SPECIFICITY: WIDELY EXPRESSED WITH HIGHEST LEVELS IN LIVER, SWALL INTESTINE, COLON, SALIVARY GLANDS, STOMACH AND APPENDIX.

SIMILARITY: CONTAINS 65 PLECTIN REPEATS.

SIMILARITY: BELONGS TO THE PLAKIN OR CYTOLINKER FAMILY.
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PPSTWSVSTMDALR-GLLPV-LGQPIIRS-IPQGIVAAWRQRSSRDPSWRQPERTILRPR
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                             GPRG-EVPAVWLLDAGIITQETLEALAQGTQS---PAQVAEQPAVKACLWGTGCVAGVLL
                                                       GGLACDLP----GRFVAESAEVLLPRLVSCPGPLDQDQQEAARAALQGGGPPYG---
                                                                                    AKDGTSLWDLLSSCHFTEEQRRGLLEDVQEGRTTVPQLLASVQRWVQETKLLAQARVMVP
                                                                                                               PQACTRFFSRITKAN-VDLLPRG----APERQRLLPAALAC---WGVRGSLLSEADVRAL
                                                                                                                                          SSSSETFPTPDGQGRTSYAQLLEECPRDETSGLHLLPLPESAPALPTEEQVQRSLQAVPG
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Eur. J. Biochem. 214:135-140(1993)
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Submitted (AUG-1996) t
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                                          use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation \cdot
                                                                                                                                                                                                                                                                                                STRAIN=GK.24;
MEDLINE=93285135; PubMed=8508785;
MEDLINE=93285135; PubMed=8508785;
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"Purification and characterization of Thermus caldophilus
                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1-21.
                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-GK24;
                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA POLYMERASE I,
PIR; S33287; S33287
                EMBL; U62584; AAB81398.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=272;
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                                                                                                                                                                                       FUNCTION: THERMOSTABLE ENZYME THAT HAS 5'-TO-3' EXONUCLEASE ACTIVITY AND NO 3'-TO-5' EXONUCLEASE ACTIVITY: CATTALYTIC ACTIVITY: N DECONVOUCLEOSIDE TRIPHOSPHATE - N PYROPHOSPHATE + DNA(N).
                                                                                                         European Bioinformatics Institute.
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SMART; SM00475; 53EXOC; 1.
SMART; SM00278; HhH1; 1.
SMART; SM00279; HhH2; 1.
SMART; SM00279; HhH2; 1.
SMART; SM00482; POLAC; 1.
PROSITE; PS00447; DNA_POLYMERASE_A; 1.
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Pfam; PF00476; DNA_pol_A;
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SEQUENCE 834 AA;
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 YGMSAHRLS---
                           RTDAVLPLTVAEVQKLLGPHVEGLKAEERH----RPVRDWILRQRQDDLDTLGLGLQGGI
                                                         QIELRVLAHLSGDENLIRVFQEGKDIHTQTASWMFGVPPEAVDPLMRR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 109.5;
Pred. No. 4.
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A851FF3C3076348E CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                -----VSTMDALRGLL----
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Best Local (
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                                                                                                                                                                                                                                     EMBL; AF075169; AF0.55702..., Helicase; DNA-binding; ATP-binding; DNP_BIND 955 962 ATP (BY CONFLICT 120 120 MISSING CONFLICT 120 157796 MW; C848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-20341310; PubMed-10880469;
MEDLINE-20341310; PubMed-10880469;
MEDLINE-20341310; PubMed-10880469;
MEDLINE-20341310; PubMed-10880469;
MEDLINE-20341310; PubMed-10880469;
MEDLINE-20341310; PubMed-10880469;
MEDLINE-20341311 S.A., Sco. Y.-S.;
"Genetic analyses of Schizosaccharomyces pombe dna2+ reveal that dna2 plays an essential role in Okazaki fragment metabolism.";
dna2 plays an essential role in Okazaki fragment metabolism.";
Genetics 155;1055-1067(2000).
                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation updat
DNA REPLICATION HELICASE DNA2.
DNA2 OR SPBC16D10.04C.
                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9URU2; Q9UUK8; 20-AUG-2001 (Re:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pasion S.G., Forsburg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (MAR-1999) to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-972;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
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                                                                    349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1054-1244 FROM N.A.
       394 KALLEVDKGHEMSPQAPRRPLPQVATLIDRFVKG----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ELONGATION AND MATURATION.
SUBUNIT: INTERACTS WITH CDC1, CDC24 AND RAD2.
SIMILARITY: BELONGS TO THE DNA2/NAM7 HELICASE FAMILY.
                                                                                                                             REI-DESLIFYKKWELEACVDAALLATQMDRVNAIPFTYEQLD------
                                     CLEIDDRVFHYKFAFLNDNGYPRNFL-HSGFSVGERVFIS---DEHGHWSLAKGHIVHIQ
                                                                  -----VLKHKLDELYPQGYPESVIQHLGY-----LFLKMSPEDIRKWNVTS----LETL
                                                                                                 REVKDEDLEFYKKWEKLLNQEERLLL--LKRGDVLTFDTEELEAYGKTLYPLYITKEDIV
                                                                                                                                                                                                                                                                                             AL035637; CAB38508.1; -. AF075169; AAC39502.1; -.
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                                                                                                                                                                       Similarity
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                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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                                                                                                                                                                          3.3%;
                                                                                                                                                                                                                                  g; ATP-binding; DNA replication.
62 ATP (BY SIMILARITY).
20 MISSING (IN REF. 1).
157786 MW; C848F4378BAD9D01 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S.L.;
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                                                                                                                                                            58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             arrell B.G., Brown EMBL/GenBank/DDBJ
                                                                                                                                                                       Score 108.5;
Pred. No. 11;
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                                                                                                                                                           Mismatches
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databases
                                                                                                                                                                                       Length 1398;
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RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zhang Q., ic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Novel genes expressed in hematopoietic stem/progenitor cells from myelodysplastic syndromes patient.";
Submitted (JUL-1999) to the EMBL/G",
-i- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUP1_HUMAN STANDARD; PRT; 476 AA. Q9Y679; Q9UNO5; Q9Y885; 20-AUG-2001 (Rel. 40, Created) 20-AUG-2001 (Rel. 40, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update) ANCIENT UBIQUITOUS PROTEIN 1 PRECURSOR.
                                                                                                                                                                                                    entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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                                                                                                                                                                                                                                                           use by non-profit institu
modified and this statement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gu J., Huang Q., Yu Y., Xu S., Han Z., Huang C., Ren S., Tu Y., Chen Z.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Hematopoietic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peng Y., Song H., Dai M., Huang Q., Mao Y., Zhang Q., Ma
Luo M., Chen J., Hu R.;
"Human ancient ubiquitous protein AUPl isoform gene.";
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1053 SIFNKRKFDYCIIDEASQIPL---PICLGP 1079
                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- TISSUE SPECIFICITY: UBIQUITOUS.
-!- SIMILARITY: BELONGS TO THE AUP1 FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
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                                                                                                                     AF100754;
AF100753;
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                                                                                          AF165515;
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Shen Y., Chen Z.
                                                       ; AAD43018.1; -.; AAD43017.1; -.; AAF86645.1; -.; AAD43010.1; -.
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                                                                                                                                                                                                                                                           is not removed
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Matches 114; Conservative
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DOMAIN
SEQUENCE FROM N.A., AND PARTIAL SEQUENCE. STRAIN-SPRAGUE-DAWLEY; TISSUE-Kidney; MEDLINE-97113037; PubMed-8942390; Ye.G.-J., Breslow E., Meister A.; "The amino acid sequence of rat kidney 5-by CDNA Cloning."
J. Biol. Chem. 271:32293-32300(1996).
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                                                                                                                                                                                                            Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                       NCBI_TaxID=10116;
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15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
5-OXOPROLINASE (EC 3.5.2.9) (5-OXO-L-PROLINASE)
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1 37 pp.
38 476 Alternative splicing.
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ANCIENT UBIQUITOUS
POLY-PHE.
                                                                                                                                                                                                            Craniata; Vertebrata; Sciurognathi; Muridae;
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J. Biol. Chem. 272:4646-4646(1997).
-i- FUNCTION: CATALYZES THE CLEAVAGE OF
GLUTAMATE COUPLED TO THE HYDROLYSIS
PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF01968; Hydantoinase_A;
Pfam; PF02538; Hydantoinase_B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hydrolase.
SEQUENCE
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InterPro; IPR003692; Hydantoinase_B.
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hes 140;
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PHOSTHATE + L-GLUTAMATE.
SUBUNIT: HOMODIMER.
TISSUE SPECIFICITY: WELL EXPRESSED IN TESTIS, K
SIMILARITY: BELONGS TO THE OXOPROLINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                               LSEADVRALGGLACDLPGREVAESAEVLLPRLVSCPGPLDQDQQEAARAALQGGGPPY--
VEPGCQAEVTDTGDI-RISVGAEGPSMADTRLDPIQLSIF--
                                                             LQLE-DTPKIQTGPPHVEKVTQCYFEGGYQETPVYLLGELGYGHQLQGPCLIIDNNSTIL
                                                                                                                                                             ETLKALLEVDKGHEMSPQAPRRP----
                                                                                                                                                                                              SLSYTPETFAQLDQRLSRLEEQCVDALQVQGFPRSQISTESFLHLRYQGTDC
                                                                                                                                                                                                                               RVNAIPFTYEQLDVLKHKLDE-----LYPQGYPESVIQHLGYLFLKMSPEDIRKWNVTSL
                                                                                                                                                                                                                                                              ----AHVLACFGGAGGQHACAIARALGMDTVHIHRHSGLLSALGLALADVVHEAQEPC
                                                                                                                                                                                                                                                                                           PRFRREVEKTACPSG------KKAREIDESLIFYKKWELE----ACVDAALLATQMD
                                                                                                                                                                                                                                                                                                                             FLTNGPCPASQLSLEEVAMGFVRVANEAMCRPI ---- RALTQARGHDPS---
                                                                                                                                                                                                                                                                                                                                                              ----GPPSTWSVSTMDALRGLLPVLGQPIIRSIPQGIVAAWRQRSSRDPSWRQPERTILR
                                                                                                                                                                                                                                                                                                                                                                                                                                                               RSGLFVVGPESAGAHPGP-ACYRKGGPVTVTDANLV-----LGRLLPASFPC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -DLLLFLNPD---AFSGPQACTRFFSRITKANVDLLPRGAPERQRLLPAALACWGVRGSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STDVSRYAGEFEHVFEASTA----GVTLQAPQL------DINTVAAGGGSRLFF
                             ----CSLSPEELSSVPPSSIWAVRPQDLDT-CDPRQLDVLYPKARLAFQNMNGSEYFVKI
                                                                                                -QLDKDT
                                                                                                                               ----ALMVSAHQHPATACSPRAGDFGAAFVERYMREFGFIIPERPVVVDDVRVRGTGRSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1288 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ERVRELAVALAQKNVKLSTEQLRCLAHRLSEPPEDLDALPL------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               137746 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IS THE CLEAVAGE OF 5-OXO-L-PROLINE TO FORM TO THE HYDROLYSIS OF ATP TO ADP AND INORG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 107.5;
Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                -----IFGPGEDQPLSPEASRKALEAVAMEVNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                             PGYL
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DR RESERVE AND SERVE AND S
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_STANDARD; PRT; 3567 AA.

(03132; 054096;

01-OCT-1993 (Rel. 27, Created)

01-OCT-1998 (Rel. 27, Last sequence update)

15-JUL-1998 (Rel. 36, Last anotation update)

ERYTHRONOLIDE SYNTHASE, MODULES 3 AND 4 (EC 2.3.1.94) (ORF 2)

DEOXYERYTHRONOLIDE B SYNTHASE II) (DEBS 2).
                                 EMBL; M63677; AAA26494.1;
EMBL; X62569; CAA44448.1;
HSSP; P28304; 1QOR.
                                                                                                                                                                                                       use by non-profit institutions as long as modified and this statement is not removed. \ensuremath{\mathsf{U}}
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      InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bevitt D.J., Cortes J., Haydock S.F., Leadlay P.F., "6-Deoxyerythronolide-B synthase 2 from Saccharopolyspora Cloning of the structural gene, sequence analysis and infe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=92155230; PubMed=1740151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Science
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MEDLINE=91220065; PubMed-2024119;
Donadio S., Staver M.J., McAlpine
Publication of genes re
Modular organization of genes re
biosynthesis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharopolyspora.
NCBI_TaxID=1836;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saccharopolyspora erythraea (Streptomyces erythraeus). Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Actinomycetales; Pseudonocardineae; Pseudonocardiaceae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COFACTOR: NADP; CONTAINS 2 COVALENTLY PATHWAY: COMPLEX POLYKETIDE FORMATION
                                                                                                                                                                                                                                                             ween the Swiss Institute of Bioinf
European Bioinformatics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                              MISCELLANEOUS: BIOSYNTHESIS OF POLYKETIDES; ACYLTRANSFERASE (AT).
BETA-KETOACYL CARRIER PROTEIN SYNTHASE (KS), AND ACYL CARRIER
PROTEIN (ACP) FOR CHAIN ELONGATION. BETA-KETOREDUCTASE (KR),
DEHYDRATASE (DH), AND ENOYL REDUCTASE (ER) FOR PROCESSING OF THE
BETA CARBON, AND THIOESTERASE (TE) FOR RELEASE AND LACTONIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MISCELLANEOUS: IN EACH ORF OF ERYA TWO MODULES ARE PRESENT EACH ENCODING FOR A FUNCTIONAL SYNTHASE SUBUNIT. THUS ERYA SHOWING 3 ORFS CODES FOR 6 SYNTHASE SUBUNITS. IT IS SUPPOSED THAT EACH SYNTHASE PARTICIPATES IN ONE OF THE SIX FAS-LIKE ELONGATION STEPS REQUIRED FOR FORMATION OF THE POLYKETIDE. MODULE 1, 2, 3, 4, 5, AND 6 PARTICIPATING IN BIOSYNTHESIS STEPS 1, 2, 3, 4, 5, AND 6,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CATALYTIC ACTIVITY: 6 METHYLMALONYL-COA + PROPIONYL-COA =
                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 + 6-DEOXYERYTHRONOLIDE B.
                                                                                                                                                                                                                                                                                      SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESPECTIVELY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J. Biochem.
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                                                                                                                                                                                                                                                                                                                                                                                                                  THE FULL-LENGTH CHAIN.
                                                                                                                                                 an email to license@isb-sib.ch).
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                                                                                                                                                                            requires a license agreement
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hem. 204:39-49(1992).
                                                                                                                                                                                                                                                                                                                                                                                TO FATTY ACID SYNTHASE (FAS).
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      Acyltransf_domain
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                                                                                                                                                                         (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                 There are no resur-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Swanson S.J., Katz L.; for complex polyketide
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pfam; pF00107; adh_zinc; 1.
pfam; pF00109; ketoacyl-synt; 2.
pfam; pF00550; pp-binding; 2.
                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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                                       KHKLDELYPQGYPESVIQHLGYLFLKMSPEDIRKWNVTSLETLKA---
                                                                                                                                                                                                                                                                       WPAGERP
                                                                                                                                                                                                                                                                                         WSCGDRPGSLLFLLFSLGWVHPARTLAGETGTESAPLGGVLTTPHNISSLSPRQLLGFPC
                                                                                                     KL--LDVVRGDGGPDPHERVDVL-QPVLFSIMVSLAELWRAHG----
                                                                                                                         SVSTMDALRG--
                                                                                                                                              LVFPGQGAQWVGMARDLLESSEVFAESMSRCAEAL --
                                                                                                                                                               RALGGLACDLPG---RFVAESAEVLLPRLVSCPGPLDQDQQEAARAALQGGGPPYGPPSTW
                                                                                                                                                                                     TLATGRARFDVRAAVLGDDRAGVCAELDALAEGRPSADAVAPVTSA--
                                                                                                                                                                                                                             AEQEAARTER-GPLPFVLSGRSEAVVAAQARALAEHLRDTPE---
                                                                                  FRREVEKTACPSGKKAREIDESLIFYKKWELEACVDAALLATQMDRVNAIPFTYEQLDVL
                                                                                                                                                                                                                                                AEVSGLSTERVRELAVALAQKNVKLSTEQLRCLAHRLSEPPEDLDALPLDLLLFLNPDAF 129
                     -LRELDDQG---
                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PS50075;
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 --LLEVD--
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IPR000794; Ketoacyl-synt.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PHOSPHOPANTETHEINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Multifunctional
                                                                                                                                                                                                                                                                                                                       3.3%;
                                                                                                                                                                                                                                                                                                                                                                374413
                                                                                                                         -LLPVLGQPIIRSIPQGIVAAWRQRSSRDPSWRQPERTILRPR
KGHEMSPQ--APR--RPLPQVATLIDRFVKGRGQLDKDTLDT
                     GMVSVGASRDE-----LETVLARWDGRVAVAAVNGPG
                                                                                                                                                                                                                                                                                                               63;
                                                                                                                                                                                                                                                                                                                                                               MW; F
                                                                                                                                                                                                                                                                                                                                                                        R -> A (IN REF. 2).
T -> S (IN REF. 2).
L -> F (IN REF. 2).
G -> V (IN REF. 2).
                                                                                                                                                                                                         -ANVDLLPRGAPERQRLLPAALACWGVRGSLLSEADV
                                                                                                                                                                                                                                                                                                                      Score 107.5;
Pred. No. 49
                                                                                                                                                                                                                                                                                                                                                                                                                   PHOSPHOPANTETHEINE
                                                                                                                                                                                                                                                                                                                                                                                                                            NADP (KR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                ACYL-ENZYME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PHOSPHOPANTETHEINE (BY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEHYDRATASE/ENOYLREDUCTASE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NON-FUNCTIONAL).
ACYL CARRIER (ACP) 1.
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BETA-KETOACYL RE
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                                                                                                                                                                                                                                                                                                                       No. 49;
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SE (AT) 1.
                                                                                                                                                                                                                                                                                                                                 DB 1;
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Q03157;
Q1-OCT-1993
                                                                                                                                                                                                                                                      the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                   TRANSMEM
DOMAIN
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                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
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01-JUN-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Solomon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=93066322; PubMed=1279693;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Brain,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus
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  CARBOHYD
               CARBOHYD
                          DOMAIN
                                       DOMAIN
                                                                                          CHAIN
                                                                                                                Glycoprotein;
                                                                                                                          PROSITE; PS00319; A4_EXTRA; 1.
PROSITE; PS00320; A4_INTRA; 1.
                                                                                                                                                                   Pfam; PF02177; A4_EXTRA; 1. PRINTS; PR00203; AMYLOIDA4.
                                                                                                                                                                                           MGD; MGI:88046; Aplp1.
InterPro; IPR001868; A4_APP.
                                                                                                                                                                                                                                 EMBL; L04538; AAA37247.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       'Identification of a mouse brain cDNA that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                579
                                                                                                                                                                                                                                                                                                                                                                                    the Alzheimer disease-associated amyloid beta protein precuoc. Natl. Acad. Sci. U.S.A. 89:10758-10762(1992).
- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. MAY BE PROTING THE GOLGI COMPLEX; HOWEVER, IT IS NOT YET CLEAR WHETER
                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: BELONGS TO THE APP FAMILY.
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                                                                                                                                                        SM00006;
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(Rel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Mouse)
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                                                                                                                  Transmembrane;
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                                                                                                                                                     A4_EXTRA; 1.
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Rodentia;
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                       AMYLOID-LIKE PROTEIN 1.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
CLATHRIN-BINDING (POTENTIAL).
POLY-GLU.
 N-LINKED
                                                                                                                Signal
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(GLCNAC. .
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RESULT 11
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Best Local
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01-JUN-1994 (Rel. 2
20-AUG-2001 (Rel. 4
HYPERSENSITIVITY RE
   MEDINE-9310711; PubMed-8316211;
Gough C.L., Genin S., Lopes V., Boucher C.A.;
Gough C.L., Genin S., Lopes V., Boucher C.A.;
"Homology between the HrpO protein of Pseudomonas solanacearum and bacterial proteins implicated in a signal peptide-independent secretion mechanism.";
secretion mechanism.";
MOI. Gen. Genet. 239:378-392(1993).
-i- FUNCTION: INVOLVED IN THE SECRETION OF A PROTEINACEOUS ELICITOR THE HYPERSENSITIVITY RESPONSE IN PLANTS (BY SIMILARITY).
                                                                                                                                                                                                                                                                 01-JUN-1994
01-JUN-1994
20-AUG-2001
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P35656;
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                                                                                                                                SEQUENCE FROM N.A. STRAIN-GMI1000;
                                                                                                                                                                                                                         Burkholderia solanacearum
                                                                                                                                                                           NCBI_TaxID=305;
                                                                                                                                                                                                        Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                      570
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SUBCELLULAR LOCATION:
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INTEGRAL MEMBRANE
                                                                                                                                                                                                          beta
                                                                                                                                                                                                                                                     SECRETION
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                                                                                                                                                                                                                         (Pseudomonas
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Pred. No. 5.
                                                                                                                                                                                                                                                                                                                                                                                                      --REALSGLLIMGAGGGSLIVLSLLL
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                                                                                                                                                                                                        subdivision; Ralstonia
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                                                                                                                                                                                                                         solanacearum).
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PROTEIN.
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                                                                                                                                                                                                        group;
                                                                                                                                                                                                                                                                                                                                                                                                      605
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MEMBRANE
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RESULT
PKN1_MY
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Best Local
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                                                                  PKN1_MYXXA
P33973;
O1-FEB-1994
O1-FEB-1994
                                                                                                                                        _MXXXA
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TRANSMEM 14
TRANSMEM 48
                   PKN1
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TRANSMEM
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                                01-FEB-1994 (Rel. 28, Creatéd)
01-FEB-1994 (Rel. 28, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
SERINE/THREONINE-PROTEIN KINASE PKN1 (EC 2.7.1.-).
 Myxococcus xanthus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein transport; Transport; Inner membrane; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00771; FHIPEP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M99633; -; NOT PIR; S35251; S35251.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE;
                                                                                                                                                                                                              655
                                                                                                                                                                                                                                                                                621
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            189 DLPGRFVA-ESAEVLLPRLVSCPGPLDQDQQEAARA-ALQGGGPPYGPPSTWSVSTMDAL 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL).
SIMILARITY: BELONGS TO THE FHIPEP (FLAGELLA/HR/INVASION PROTEINS EXPORT PORE) FAMILY.
                                                                                                                                                                                                                                            VLPLTVAEVQKLLGPHVEGL 556
                                                                                                                                                                                                                                                                                                                                                                                                                     NMRAIL-----ESLVVWGPKEKDTLMLVEYVRGDLGRQIAHQA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                 YPESVIQHLGYLFLKMSPEDIRKWNVTSLETLKALLEV--DKGHEMSPQAPRRPLPQVAT 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SGKKAREIDESLIFYKKWELEACVDAALLATQMDRVNAIPFTYEQLDVLKHKLDELYPQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DAALSATGQRVERVIADHVVHVLRRSAHLFVGLQETQWMLERVTTDYPGLVAEAQK-AVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RGLLPVLGQPIIRSIPQGIVAAWRQRSS-----RDPSWRQPERTILRPRFRREVEKTACP 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DIPGEPVAVPDGHLLIP-------DLPEALRAQAVEAAGLPNHPAPHWIAPAHVAQ 467
                                                                                                                                                                                                            -----RYVRRMIEPHLQAL 668
                                                                                                                                                                                                                                                                                                             RQLDVLYPKARLAFQNMNGSEYFVKIQSFLGGAPTEDLKALSQQNVSMDLATFMKLRTDA
                                                                                                                                                                                                                                                                                                                                                                                 LIDRFVKGRGQLDKDTLDTLTAFYPGYLCSLSPEELSSVPPSSIWAVRPQ---DLDTCDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PR00949; FLGBIOSNFLHA.; PS00994; FHIPEP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPR001712; Bact_exp_FHIPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  104
196
229
291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -; NOT_ANNOTATED_CDS
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                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36
72
128
216
253
315
315
73990 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3.3%;
19.2%;
                                                                                                                                                                                                                                                                                ---IMRLRGIMQGNPVETPSALA----IVTSMDIR---
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                                                                                                                                                                                                                                                                                                                                                ---PAILLDLSVEQ-----TVRQAIKPTPAGNFLTLDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 106; DB Pred. No. 6.3;
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DA6FA8F32417E4D2 CRC64;
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                                                                                                                        PRT;
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                                                                                                                        693
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 690;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Phosphorylation.
DOMAIN 59.
NP_BIND 65
BINDING 88
ACT_SITE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MUTAGEN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Munoz-Dorado J., Inouye S., Inouye M.;
"A gene encoding a protein serine/threonine kinase is required for normal development of M. xanthus, a gram-negative bacterium.";
Cell 67:995-1006(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entitles requires a license agreement (See http://www.isb-or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR002290; Ser_thr_kin_actsite
InterPro; IPR001440; TPR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; A41090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M73498; AAA25402.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; delta subdivision; Myxobacteria; Myxococcales; Cystobacterineae; Myxococcaceae; Myxococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00069; pkinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- FUNCTION: PLAYS AN ESSENTIAL ROLE IN PROPER TIMING OF EARLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=34;
                                   607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro;
                                                                                                                                                                          492
                                                                                                                                                                                                                                            433
                                                                                                                                                                                                                                                                                                              378
                                                                                                                                                                                                                                                                                                                                                157 RQRLLPAALACWGVRGSLL------SEADVRALG-GLACDLPGRFVAESAEVLLPR 205
 374
                                                                                                                                                                                                        254
                                                                                                                                                                                                                                                                              206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PTM: AUTOPHOSPHORYLATED. SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DEVELOPMENTAL STAGE: DEVELOPMENTALLY REGULATED TO START IMMEDIATELY BEFORE SPORE FORMATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENZYME REGULATION: MAY BE REGULATED BY CALCIUM OR A CALMODULIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LIKE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEVELOPMENT EVENTS.
                                                                                                                                                                                                                                                                            LVSCP-----GPLDQDQQEAARAALQGGGPPYGPPSTWSVSTMDA---LRGLLPVL--
                                                                                                                                                                                                                                                                                                              QRRLAPAAPAV -- PRASLVEVPVQVVLRPGESPVRLRGSGLS---RGGLFLHGGRVLPPL 432
 --FLKMSPEDIRKWNVTSLETLKALLEVDKGHEMSP
                                                                  LLATQMDRVNAIPFTYEQLDVLKHKLDELYPQ--GYPESVIQHLGYL-
                                                                                                                                                                                                                                          CSRLPVVLELASGPLSV-MCEVVRVVPPAQARVWGMPTGFGVQFVEATAVLKAAVDALLQ 491
                                                                                                      ESLEQHSLTPPQRAQVDALRV - - -
                                                                                                                                        -QPERTILRPRFRREVEKTACPSGKKAREIDESL-----IFYKKWE-----LEACVDAA
                                                                                                                                                                        GEP-VRAVPQVPLTEDPAVARLLEAWRQRSAGDAYAVLALEPDSDMGTVRLRTREAWRSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q63450;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PS50011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PS00108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPR000719;
                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A41090.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Serine/threonine-protein kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROTEIN_KINASE_ST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROTEIN_KINASE_ATP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROTEIN_KINASE_DOM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 328 F
73 A
88 A
180 B
88 K
74173 MW;
                                  -TAEQLESLRREFLARRPQAMGTARSHFQSGGALERDGQLSQALDQY
                                                                                                                                                                                                                                                                                                                                                                                                 3.2%;
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                                                                                                                                                                                                        -GIVAAWRQRSSRD--
                                                                                                                                                                                                                                                                                                                                                                                 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
K-N: LOSS OF ATP-BINDING.
W; ED532EABF7215A91 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                 Score 105;
Pred. No. 7

    RVREAAEALGATVQRALYDAWRGNHRGVAKCLEAG

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                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                               Length 693,
                                                                                                                                                                                                                                                                                                                                                                                  Indels 114;
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DPO1_THETH
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Best Local S
Matches 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF01367; 5_3_exonuclease; 1.
Pfam; PF00476; DNA_PO1_A; 1.
PRINTS; PR00868; DNAPOLI.
SMART; SM00475; 53EXOC; 1.
SMART; SM00278; HhH1; 1.
SMART; SM00279; HhH2; 1.
SMART; SM00279; HhH2; 1.
SMART; SM00482; PC1Ac; 1.
SMART; SM00482; PC1Ac; 1.
PROSITE; PS00447; DNA_POLYMERASE_A; 1.
PROSITE; PS00447; DNA_POLYMERASE_A; 1.
Transferase; DNA-directed DNA polymerase; DNA replication; DNA repair; NA-h104ing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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P52028;
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
DNA POLYMERASE I, THERMOSTABLE (EC 2.7.7.7) (TTH POLYMERASE 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR002421; 5_3_exonuclease.
InterPro; IPR002298; DNA_pol1.
InterPro; IPR001098; DNA_pol_A.
InterPro; IPR000513; Exo_N_I.
InterPro; IPR003583; HHH_1.
InterPro; IPR003584; HHH_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Cloning, nucleotide sequence, and expression in Escherichia coli of DNA polymerase gene (polA) from Thermus thermophilus HB8.";
J. Ferment. Bioeng. 76:265-269(1993).
-I- CATALYTIC ACTIVITY: N DEOXYNUCLEOSIDE TRIPHOSPHATE -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; D28878; BAA06033.1; -. HSSP; P19821; 1TAU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Urabe I.;
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STRAIN-HB8 / ATCC 27634;
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Bacteria; Thermus/Deinococcus group; Thermus group; Thermus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
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                                                         147 VDLLP--RGAPERQRLLPAALACWGVRGSLLSEAD-----VRA-----LG
       192
                                                                                                                                                                                                                                                                                                                                                                                                            y Match 3.2%; Score 104.5; Local Similarity 19.3%; Pred. No. 11; hes 142; Conservative 81; Mismatches
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                                                                                                                                    -----RILTADRDLYQLVSDRVAVLHPEGHLITPEWLWEKYGLRPEQWVDFRALVGDPS 191
                                                                                                                                                                                                                                                                           GRAPTPEDF----PRQLALIKELVDLLGFTRLEVPGYEAD---DVLATLAKKAEKEGYEV 137
                                                                                                                                                                                                                                                                                                                                               GVLTTPHNISSLSPRQ------LLGFPCAEVSGLSTERVRELAVALAQKNVKLSTEQ 98
   -DNLPGVKGIGEKTAL--KLLKEWGSLENLLKNLDRVKPENVREKIKAHLEDLRLSLELS 248
                                                                                                                                                                                                       LRCLAHRLSEPPEDLDALPLDLLLFLNPDAF-----SGPQACTRFFSRITKAN 146
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834 AA; 94049 MW; 1A98145DC11A54A9 CRC64;
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"Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trachomatis."; Science 282:754-759(1998).	W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,	'UW-3/CX; D C Kalman C Tammal C T Ear T Maratha B Arawind		yl-tRNA synthetase of Chlamydi iol. 177:5179-5185(1995).	M.J., Yasin B., Pang M.;	IN=L2/434/BU;		eria; Chlamydiale _TaxID=813;	hlamydia trachomatis.	YNTHETASE BETA CHAIN (GLYCINETRNA LIGASE BETA CHAIN)].	GLYCYL-TRNA SYNTHETASE (EC 6.1.1.14) (GLYRS) [INCLUDES: GLYCYL-TRNA SYNTHETASE ALPHA CHAIN); GLYCYL-TRNA	0-MAY-2000 (Ref. 39, Last sequence update) 0-AUG-2001 (Ref. 40, Last annotation update)	1-NOV-1997 (Rel. 35, Created)	YG_CHLTH 46371; C	14 LTR	718 KRGYVETLFG 727		673 YGMSAHRLSQELAIPYEEAVAFIERYFQSFPKVRAWIEKTLEEGR 717	LLGPHVEGLKAEERHRPVRDWIL	615 QIELRVLAHLSGDENLIRVFQEGKDIHTQTASWMFGVPPEAVDPLMRRAAKTVNFGVL 672	Ϋ́	567NOTATATGRLSSSDP-NLQNIPVRTPLGQRIRRAFVAEAGWALVALDYS 614	427 GRGQLDKDTLDTLTAFYPGYLCSLSPEELSSVPPSSIWAVRPQDLD 472	535 LQHRELTKLKNTYVDPLPSLVH	QHLGYLFLKMSP	475 EVFRLAGHPENLNSRDQLERVLEDELRLPALGKTQKTGKRSTSAAVLEALREAHPIVEKI 534	IPFTYEQLDVLKHKL-DELYPQG	415 HRNILKRIEGEEKLIWIYHEVEKPISRVIAHMEATGVRRDVAYIQALSIEIAEEIRRIEE 474	- mi	359 AVLASREGLDLVPGDDPMLLAYLLDPSNTTPEGVARRYGGEWTEDAAHRALLSERL 414	LGQPIIRSIPQGIVAAWRQRSSRDPSWRQPERT	303PPEGAFVGFVLSRPEPMWAELKALAACRDGRVHRAADPLAGLKDLKEVRGLLAKDL 358	3	:	185 GLACDLPGRFV-AESAEVLLPRLVSCPGPLDQDQQEAARAAL 225

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PROSITE; PS00339; AA_TRNA_LIGASE_II_2; 1.
Aminoacy1-tRNA synthetase; Protein biosynthesis;
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Pfam; PF02092; tRNA_synt_2f; 1.
PRINTS; PF00104; TRNASYNTHGB.
PRINTS; PR01045; TRNASYNTHGB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AE001352; AAC68391.1;
InterPro; IPR002310; AR_tRNA_ligase_II.
InterPro; IPR002310; tRNA_synt_2e.
InterPro; IPR002311; tRNA_synt_2f.
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540 RRAIIKQGLQNLTGDQIVAIAPEHLIDETVFLTEHPFVISAQFDPAFCSLPKELLIAEMI
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                             321 LEACVDAALLATQMDRVNAIP---
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SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.
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                                                                                                                                                                                                  APERQRLLPAALACWGVRGSLLSEADVRALGGLACDLPGRFVAESAEVL---LPRLVSC-
                                                                                  VAAWRQRSSRDPSW--RQ-PERTILRPRFRREVE--KTACPSGKKAREIDESLIFYKKWE
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                                                                                                                                            --PGPLDQDQQEAARAALQGGGPPYGPPSTWSVSTMDALRG--LLPVLGQPIIRSIPQGI
                                                                                                                                                                                                                                                          LSTEQLRCLAHRLSEPPEDLDALPLDLLLFLNPDAFSGPQACTRFFSRITKANVDLLPRG
                                                         V-----SGNTSWGHRQLDNRQLTIPSSNMYVDTLRSAC
                                                                                                                                                                        ALDQ----PSAI--WRVR-----SINGTDYLFLVIPEE-RKETAAILVNELPQLIRSI
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Similarity 21.4%;
30; Conservative 7
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GLYCYL-TRNA SYNTHETASE BETA CHAIN.
T -> A (IN SEROVAR L2).
D -> G (IN SEROVAR L2).
F -> S (IN SEROVAR L2).
S -> P (IN SEROVAR L2).
S -> P (IN SEROVAR L2).
I -> V (IN SEROVAR L2).
I -> V (IN SEROVAR L2).
I -> V (IN SEROVAR L2).
J -> P (IN SEROVAR L2).
J -> P (IN SEROVAR L2).
S -> N (IN SEROVAR L2).
G -> L (IN SEROVAR L2).
G -> D (IN SEROVAR L2).
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Pred. No. 15;
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Homo sapiens (Human).

Larvota; Metazoa; Chordata; A
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Alwazzan M., Hamshare M.G., Lenno
"Six transcripts map within 200 k
expanded repeat.";
Mamm. Genome 9:485-487(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUB-Colon carcinoma;
MEDLINE-96354916; PubMed-8769423;
Keon B.H., Schaefer S., Kuhn C., Grund C.,
"Symplekin, a novel type of tight junction
J. Cell Biol. 134:1003-1018(1996).
                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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SUBCELLULAR LOCATION: CYTOPLASMIC
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                                                                                                                                                                      DETECTED IN STOMACH, DUODENUM, PANCREAS, LIVER, FETAL BRAIN, CARCINOMAS, LENS-FORMING CELLS, FIBROBLASTS, LYMPHOCYTES, LYMPHOMA CELLS, ENTHHROLEUKEMIA CELLS BUT NOT IN ENDOTHELIUM OF VESSELS, EPIDERMIS, INTERCALATED DISKS, PURKINJE FIBER CELLS OF THE HEART
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(Rel. 40, Last annotation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U49240; AAC50667.1; -.
EMBL; V10931; CAA71861.1; -.
MIM; 602388; -
Cell adhesion; Tight junction; Nuclear protein.
DOMAIN 213 228 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
DOMAIN 709 712 POLY-LEU
DOMAIN 709 1043 POLY-SER.
SEQUENCE 1142 AA; 126499 MW; 46FFIB4C561C4409 GRC64;
                               524 MDLATEMKLRTDAVLPLTVAEV-QKLLG-PHVEGLKA 558
                                                                                                                                                                                                                                                   408 QAPRRPL----PQVATLIDRFVKGRGQLDKDTLDTLTAFYPGYLCSLSPEELSSVPPSSI 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                  308 EIDESLIF----YKKWELEACVD-------AALLATQMDRVNAIPFTYEQL 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     375 SSMSPLEEEAPQAKRRPEPIIPVTQPRLAGAGGRKKIFRLSDVLKPLTDAQVEAMKLGAV 434
                                                                                                                                                 464 WAVRPQDLDTCDPRQLDVLYPKARLAFQNMNGSEYFVKIQSFLGGAPTEDLKALSQQNVS 523
                                                                                                                                                                                                    696 EQPIRGMGMNSPELLLLVENCPKGAETLVTRCLHSLT------DKVPPSPE 740
                                                                                                                                                                                                                                                                                                                                                     348 DVLKHKLDELYPQGYPESVIQHLGYLFLKMSPEDIRKWNVTSLETLKALLEVDKGHEMSP 407
                                                                                                                                                                                                                                                                                                                                                                                                          596 VRSQALLFIKRMYEKEQLREYVEKFALNYLQLLVHPNPPSVLFGADKDTEVAAPWT---- 651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          541 LITESALEVVRKYCEDESRTYLGMSTLRDLIFKRPSR-----QFQYLHVLLDLSSHEKDK 595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 491 LYQEYNAYLAAGASGSLDKY------EDCLIRLLSGLQEKPDQKDGIFTKVVLEAP 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 213 LDQDQQEAARAALQGGGPPYGPPSTWSVSTMDALRGLLP------VLGQP 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   435 KRILRAEKAVACSGAAQVRIKILASLVTQFNSGLKAEVLS-FILEDVRA---RLDLAFAW 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   156 ERORLLPAALACWG---VRGSLLSEADVRALGGLACDLPGREVAESAEVLLPRLVSCPGP 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        122 LFLNPDAFSGPQACTR---------FFSRITKANVDLLPRGAP 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          317 LARLMATQMTAAGLGPGVEQTKQCKEEPKEEKVVKTESVLIKRRLSAQGQAISV--VGSL 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         257 ISGOSDTDITAEFLOPLLTPDNVANLVLISMVYLPEAMPASFQAIYTPVESAGTEAQIKH 316
773 QALPKLIKLN-----PIVVKEVFNRLLGTQHGEGNSA 804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83 LAVALA------QKNVKLSTEQLRCLAHRLSEPPEDLDALPLDLL 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35 LAGETGTE-SAPLGGVLTTPHNISSLSPRQLLGFPCA-----EVSGLSTE-RVRE 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IIRSIPQGIVAAWRQRSS------RDPSWRQPERTILRPRFRREVEKTACPSGKKAR 307
                                                                                                                                                                                                                                                                                                        -----EETVKQCLYLYLALLPQNHKLIHELAAVYTEAIADIKRTVLRVI 695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82; Mismatches 231; Indels 202; Gaps
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Search completed: December Job time: 53 sec 7, 2001, 09:48:50

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Result
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Listing first 45 summaries
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Perfect score:
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2: sp_bacteria
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Match
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Gapop 10.0 , Gapext 0.5
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3261
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  GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
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sp_mhc:*
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1643.568 Million cell updates/sec
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                   QSugs3 homo sapien
QSwxj0 corynebacte
Q32836 pelargonium
Q15029 homo sapien
Q9p0a9 homo sapien
Q9s126 arabidopsis
Q9ab4 arabidopsis
Q9ab4 arabidopsis
Q9u5y1 dictyosteii
Q7503 homo sapien
Q9w5a4 drosophila
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Q14859 homo sapien
O9btr2 homo sapien
O9era7 rattus norv
Q61468 mus musculu
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Q9f1j5
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pseudomonas
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106	106	107	107	107.5	108	108	108.5	108.5	108.5	108.5	109	110	110	110.5	111	111	111	111.5	111.5	111.5	112.5	112.5	113.5	113.5	114
ω ω	3.3	ω ω	ω . υ	ω ω	ω ω	ω	ω ω	3. 3	3. 3	ω	ω ω	3.4	3. <u>4</u>	3.4 4	3.4	3.4	3.4	3.4	3.4	ω .4	3.4	3.4	ω .5	3.S	ω .5
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. Q9rwv6 deinococcus	Q9z360 streptomyce	Q9glm4 bos taurus	Q9a844 caulobacter		Q9h5z2 homo sapien	Q9pd02 xylella fas	Q94226 caenorhabdi	Q9uru2 schizosacch	Q9hta6 pseudomonas	Q9d0c6 mus musculu	Q9xah6 streptomyce	Q50857 myxococcus	Q9k3y2 streptomyce	022706 arabidopsis	Q9upa5 homo sapien	O43161 homo sapien	Q9i8el fugu rubrip	O14686 homo sapien	O14687 homo sapien	Q9w8x7 porcine ade	Q9ukv7 homo sapien		095712 homo sapien	Q9nk99 drosophila	Q9y1t2 drosophila

ALIGNMENTS

Qy	Фр	Qу Дъ	Qy Db	Quer Best Matc	RA RA SQ	2000	G D D D D A	RESULT Q9BR17 ID Q
239 SVSTMDALRGLLPVLGQPIIRSIPQGIVAAWRQRSSRDPSWRQPERTILRPRFRREVEKT 298	179 DVRALGGLACDLPGREVAESAEVLLPRLVSCPGPLDQDQOGEAARAALQGGGPPYGPPSTW 238 	119 DLLLFLNPDAFSGPQACTRFFSRITKANVDLLPRGAPERQRLLPAALACWGVRGSLLSEA 178 	LSPRQLLGFPCAEVSGLSTERVRELAVALAQKNVKLSTEQLRCLAHRLSEPPEDLDALPL	yo.4*; Score 3110; D8 4; Length 630; Best Local Similarity 96.5*; Pred. No. 2.9e-230; Matches 608; Conservative 4; Mismatches 16; Indels 2; Gaps MALQRLDP-CWSCGDRP-GSLLFLLFSLGWVHPARTLAGETGTESAPLGGVLTTPHNISS 58	SEQUENCE FROM N.A. SEQUENCE FROM N.A. SEQUENCE FROM N.A. CODLEY V.; SUBMITCED (APR-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AL031258; CAC37289.1; - SEQUENCE 630 AA; 68985 MW; FA17E3609B6CC9CA CRC64;	Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9806;	01-JUN-2001 (TrEMBLrel. 17, Created) 01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) C335H7.1 (MESOTHELIN). MSLN.	LT 1 17 17 PRELIMINARY; PRT; 630 AA.

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Q9W5A4 Q9L8H4

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Best Local Similarity
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Q14859;
01-NOV-1996
01-NOV-1996
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE-95394969; P. Kojima T., Oh-eda M Yamaguchi N.;
                                                                                                                                                                                                                                                                                                                                            CHAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                 Signal.
SIGNAL
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EMBL; D49441; BAA08419.1; .
InterPro; IPR000585; Hemopexin.
PROSITE; PS00024; HEMOPEXIN; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 17, Last annotation update)
PRE-PRO-MEGAKARYOCYTE POTENTIATING FACTOR PRECURSOR
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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622 /
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286
68037
                                                                                                                                                                                                                                                            93.7%;
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                                                                                                                                                                                                                                     Score 3055; DB 4;
Pred. No. 4.8e-226;
3; Mismatches 16;
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MEGAKARYOCYTE POTENTIATING
, 1F0FE52883CA6C13 CRC64;
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Q9BTR2;
Q9BTR2;
01-JUN-2001
01-JUN-2001
01-JUN-2001
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TISSUS-PANCREATIC ADENOCARCINOMA;
TISSUS-PANCREATIC ADENOCARCINOMA;
Strausberg R.;
Strausber
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Homo sapiens (Human).
Homo sapiens (Human).
'``rvota; Metazoa; Chordata; '
'`rvota; Primates;
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Pred. No. 4.3e-225;
4; Mismatches 15;
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Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yamashita Y., Yokoyama M., Kobayashi E., Takai S., Hino O.;
"Mapping and determination of the cDNA sequence of the Erc of preferentially expressed in renal cell carcinoma in the Tsc: mutant (Eker) rat model.";
Biochem. Biophys. Res. Commun. 275:134-140(2000).
EMBL; D87351; BAB13512.1;
EMBL; D87351; BAB13512.1;
SEQUENCE 625 AA; 68852 MW; 343EF77ADF390CD2 CRC64;
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                                                   LPLDLLLFLNPDAFSGPQACTRFFSRITKANVDLLPRGAPERQRLLPAALACWGVRGSLL 175
                                                                                                   MALPTAQPLIGSCGSPICSRSFLLLLLSLGWLPLLQTQTTRTSQEAALLHAVTGTV-DFA
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55.9%;
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                                                                                                                                                                                                                                                                                                                          Score 1710; DB 11;
Pred. No. 8.2e-123;
80; Mismatches 184;
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Matches 352; Conserv
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Q61468;
O1-NOV-1996
O1-NOV-1996
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                                                                                                                                                                            Signal.
SIGNAL
SEQUENCE
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MSLN.
Mus musculus (Mouse).
Mus musculus (Mouse).
Metazoa; Chordata;
Metazoa; Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kojima T., Taniguchi Y., Hattori K., Oh-eda M.; "mouse Megakaryocyte Potentiating Factor cDNA."; Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                   MGD; MGI:1888992;
                                                                                                                                                                                                                                                                                                                           CDNA
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                                                                                                                                                                                                                                                                                                                                            "Molecular cloning
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                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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DFNVREAFSSGAPLLGPGFVFAWIPALLSA
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MALQRLDP-CWSCGDR--PGSLLFLLFSLGWVHPARTLAGETGTESAPLGGVLTTPHNIS
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D86370; BAA13077.1; -.
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                                                                Conservative
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69423
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                                                                                      Score 1707;
Pred. No. 1
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9A5E9C3222C6983F CRC64;
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Sciurognathi; Muridae
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Murinae; Mus
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SEQUENCE
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MESOTHELIN/MEGAKARYOCYTE POTENTIATING FACTOR (FRAGMENT).
Homo sapiens (Human).
                                                                                                                            family are detectable in sera from patients with ov Proc. Natl. Acad. Sci. U.S.A. 19:11531-11536(1999). EMBL: AF180951; AAF01409.1; -.
                                                                                                                                                                                Scholler N., Fu N., Yang Y., Ye Z., Hellstroem I.;
                                                                                                       PROSITE;
                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                interPro;
                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                  Soluble member(s) of the mesothelin/megakaryocyte potentiating factor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SKWSVSTLDALQSLVAVLDESIVQSIPKDVKAEWLQHISRDPSRLGSKLTVIHPRFRRDA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SLSPRQLLGFPCAEVSGLSTERVRELAVALAQKNVKLSTEQLRCLAHRLSE--PPEDLDA 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SLVGLSVAEVQKLLGPNIVDLKTEEDKSPVRDWLFRQHQKDLDRLGLGLQGGIPNGYLVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EQKACPPGKEPYKVDEDLIFYQNWELEACVDGTMLARQMDLVNEIPFTYEQLSIFKHKLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       {\tt SEADVRALGGLACDLPGKFVARSSEVLLPWLAGCQGPLDQSQEKAVREVLRSGRTQYGPP}
                                                                                                      PS00024; HEMOPEXIN; UNKNOWN_1
                                                                                                                   IPR000585; Hemopexin
                                                                 398
398 AA;
  Conservative
                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                 398
43811 MW;
              46.8%;
97.1%;
                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                 2D542C407807C498
                                                                                                                                                                                                                                                                                                                                                                                                                 619
                                                                                                                                                                                            Goodman
                                                                                                                                                                                                                                                                                                                                                  398
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                                                                                                                                                                                            G.E.,
                                                                 CRC64;
                         Length
                                                                                                                                                      ovarian
                                                                                                                                                                                            Hellstroem
  Indels
                           398;
                                                                                                                                                        carcinoma.";
 8
                                                                                                                                                                                            K.E.,
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Score 1526; DB 4;
Pred. No. 5.6e-109;
1; Mismatches 0;
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                                                                                                                Query Match
Best Local
                                                                                                          Matches
            370
                       193
                                                           271
                                                                                  218
                                                                      97
RGLLPVL--
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-GQ---PIIRSIPQGIVAAWRQRSSRDPSWRQPERTILRPRFRREVEK

297

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20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9F1J5;
                                                                                                                                                                                                                                                                          Submitted (JAN-2001) to the EMBL/GenBank/DDBJ EMBL; AB053455; BAB20913.1; -
Interpro; IPR01712; Bact_exp_FHIPEP.
Pfam; PF00771; FHIPEP; 1
PRINTS; PR00949; TYPE3IMAPROT.
SEQUENCE. 698 AA; 75549 MW; 4868E407FCE559;
                                                                                                                                                                                                                                                                                                                                                   Takikawa Y., Eo S., Adact
"Deduced hrpo genes from
subsp. avenae."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-GM4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria;
Burkholderia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pseudomonas glumae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PUTATIVE HRPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PUTATIVE HRPO.
                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=337;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           173
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                                                                                                                                                                                                             Local Similarity
nes 135; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
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                                                   DRAWRRETLASMORVGR-KTEVPPILPRAPOFACAVGVR--
                                                                            TRFFSRITKANVDLLPRGAPERQRLLPAA - - LAC - WGVRGSLLSEADVRALGGLACDLPG
                                                                                                                                                          GMSAGDAANRFSVLSVGDAMVSQIPSLLL----SVAAGVMITRVADERQA----KQRSLGD
                                                                                                                                                                                 GETGTESAPLGGVLTTPHNISSLSPRQLLGFPCAEVSGLSTERVRELAVALAQKNVKLST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DELYPQGYPESVIQHLGYLFLKMSPEDIRKWNVTSLETLKALLEVDKGHEMSPQAPRRPL 414
----AANVAMPTLDAA----FEAERAALQEALGLPFPGITMWVHAPLPVATFEIL
                        RFVAESAEVLLPRLVSCPGPLDQDQQEAARAALQGG-GPPYGPPSTW-----SVSTMDAL
                                                                                                     E----IGHQLGSSSRALFFAAVLLLAFAIVPGFPSLLFVLLAAALSFAGYRLSVRKPSSR
                                                                                                                               EQLRCLAHRLSEPPEDLDALPLDLLLF-LNPD-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LDLSVQ 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LDLSVQ 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PQVATLIDRFVKGRGQLDKDTLDTLTAFYPGYLCSLSPEELSSVPPSSIWAVRPQDLDTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PQVATLIDRFVKGRGQLDKDTLDTLTAFYPGYLCSLSPEELSSVPPSSIWAVRPQDLDTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DELYPQGYPESVIQHLGYLFLKMSPEDIRKWNVTSLETLKALLEVNKGHEMS------
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                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                         4.1%;
23.5%;
                                                                                                                                                                                                                                                                                                                                                                    Adachi S., Kojima
from Burkholderia
                                                                                                                                                                                                                                                                                                                                                                                                                                                               beta subdivision; Burkholderia
                                                                                                                                                                                                             70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                         Score 133; DB Pred. No. 0.11;
                                                                                                                                                                                                                                                                              4B8BE407FCE559A3 CRC64
                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     869
                                                                                                                                                                                                                                                                                                                                                                   M.; glumae and Acidovorax avenae
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                                                                                                                                                                                                                                    2;
                                                                                                                                                                                                             209;
                                                                                                                                                                                                                                     Length 698
                                                                                                                               -AFSG------PQAC
                                                                                                                                                                                                             Indels 160;
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                                                  -ISPDL--
                                                                                                                                                                                                           Gaps
                                                                             192
                                                                                                                                135
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416
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QUESTION AND PROPERTY OF THE P
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Best Local Similarity
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Q9UGS3;
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DJ756G23.1 (NOVEL LEUCINE RICH PROTEIN) (FRAGMENT).
DJ756G23.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PRO0019; LEURICHPPT
SMART; SM00370; LRR; 8.
SMART; SM00082; LRRCT; 2.
SMART; SM00013; LRRNT; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF01462; LRRNT; 1. Pfam; PF01463; LRRCT; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases EMBL; AL035681; CAB63072.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00560; LRR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR003591; LRR_typ.
InterPro; IPR003592; LRR_out.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000372;
InterPro; IPR000483;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            467
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                           123
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                                                                        RLSLHHNELQALPGPV-----LSQARGLARLELGHNPLTYAGEEDGLALPGLRELLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DVLKHKLDELYPQGYPESVIQHLGYLFLKMSPEDIRKWNVTS-LETLKALLEVDKGHEMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IHDVPHLMVTMPPGKAMLPDLRLVPAEVAAA----SARSCWRWPRR-----RGRPPVDS
                                                                                                                     VSGLSTERVRELAVALAQKNVKLSTEQLRCLAH-RLSEPP-----
                                                                                                                                                                                                               RPGSL--LFLLFSLGWVHPARTLAGETGTESAPLGGVLTTPHN-ISSLSPRQLLGFPCAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -SMDIRRYVRRMIESRLGWLSVYSYQE-LGEHVE 687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NFLALPPND---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIWAVRPQDLDTCDPRQLDVLYPKARLAFQNMNGSEYFVKIQSFLGGAPTEDLKALSQQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TEYVRGDLSRF - - LAHRAAKGERQLS - - - - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PQAPRRPLPQVATLIDRFVKGRGQLDKDTLDTLTAFYPGYLCSLSPEE-----LSSVPPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DQLSHDAPGLVAEVQKVLPPQRIADVLRRLLEEQVSIRNVRSFMESLIAWGAKEKDMLML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGTPRLDRRARGAGQDAV----WRTEQIIAHRLVAPCGATATLFLGIQEVQWI-----L
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                      -----FLNPDAFSGPQACTRFFSRITKAN-VDLLP----RGAPERQRLLPAALAC----
                                                                                                                                                                     RPGTFGALGALATLNLAHNALVYLPAMAFQGLLRVRWLRLSHNALSVLAPEALAGLPALR 250
                                                                                                                                                                                                                                                                    113;
                                                                                                                                                                                                                                                                                                                                                                                                           SM00369; LRR_TYP; 4.
R 797 797
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                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                     4.08;
                                                                                                                                                                                                                                                                                                                                                                                       85614 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LRR_Cterm.
                                                                                                                                                                                                                                                                 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----AAF-----LIDRIQSFVGAAPREGVVLVT---
                                                                                                                                                                                                                                                                                        Score 131.5; D
Pred. No. 0.17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; I
Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                    8C3247883EAE59AD CRC64;
                                                                                                                                                                                                                                                               Mismatches
797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----AVLFDMQAEQHIRAAIKQTPTG
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                                                                                                                                                                                                                                                                                                            DB 4;
                                                                                                                                                                                                                                                               181;
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Best Local S
Matches 137
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Pfam; PF00694; Aconitase_C; 1.
PRINTS; PR00415; ACONITASE_
ProDom; PD000511; Aconitase; 1.
PROSITE; PS00450; ACONITASE_1; UI
PROSITE; PS01244; ACONITASE_2; 1
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SEQUENCE
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"Brevibacterium lactofermentum ATCC
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InterPro; IPR000573; Aconitase
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  232 YGPPSTW----SVSTMDALRGLL-----
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                                                                                                                                                                                                                                                                79 TPARVLMQDFTGVPC -- VVDLAT -- MREAVAA --
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                                                                                                                                                                                                                                                                                                    SPRQLL-----GFPCAEVSGLSTERVRELAVALAQKNVKLSTEQLRCLAHRLSEPPEDLD
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                                                                                                                                                                                                          AL-PLDLLL--FLNPDAFSGPQACTRFFSRITKANVDLLPRGAPERQRLLPAALACWGVR 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----RFLQV-----PGAALRALPSLFSLHLQDNAVDRLAPG
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                                                   ----SESNERVVP-----PGTGIVHQVNI---
                                                                                                     GSLLSEADVRALGGLACDLPGRFVAESAEVLLPRLVSCPGPLDQDQQEAARAALQGGGPP
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Last sequence update)
Last annotation updat
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Pred. No. 0.56
76; Mismatches
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C 13869 acn
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  -PVLGQPIIRSIPQGIVAAWRQRSSRD
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gene for Aconitase.";
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                                                                                                                                                                                                                                                                                                                                                                                                                 Length 939;
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1E HYPOTHETICAL 245.6 KDA PROTEIN.
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                                                         Matches
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Best Local
    1006
                                                                                                                                                                                                                       MEDLINE=94363755; PubMed=8082181;
MEDLINE=94363755; PubMed=8082181;
Downie S.R., Katz-Downie D.S., Wolfe K.H., Calie P.J., Palmer J.D.;
"Structure and evolution of the largest chloroplast gene (ORF2280):
internal plasticity and multiple gene loss during angiosperm
                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid Geraniales; Geraniaceae; Pelargonium.
                                                                                                                               SEQUENCE
                                                                                                                                            Hypothetical
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EMBL; M83200; AAA73173.1; -.
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RIREIS-RMCLRNLTLSAERIRRNNESPLTHTHLRSPNVLEFLYSTLLLLL----VAGYL 1060
                            RVRELAVALAQKNVKLSTEQLR-----CLAHRLSEPPEDLDALPLDLLLFLNPDAFSGPQ 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STVVPSIAGPKRPQDRILLSEAKEQFRKDLPTYTDDAVSVDTSIPATRMVNEGGGQPE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PSWRQPERTILRPRFRREVEKTACPSGKKAREIDESLIFYKKWELEACVDAALLATQMDR
                                                                       Similarity
                                                                                                                           il protein; Chloroplast.
2109 AA; 245645 MW; 948980477223DE8C
                                                         Conservative
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                                                                      3.8%;
                                                                                                                                                                     AAA_subfam.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  604
                                                         91;
                                                                      Score 125.5;
Pred. No. 2;
                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                      update)
                                                                                   DB 8;
                                                         207;
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                                                                                                                              CRC64;
                                                                                 Length
                                                         Indels
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                                                                                    2109;
                                                         199;
                                                                                                                                                                                                                                                                                                                                      Rosidae;
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01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
KIAA0312 (UPSTREAM REGULATORY ELEMENT BINDING PROTEIN
KIAA0312 OR UREB1.
                                                                                                                                                       Nagase T. Ishikwa K., Nakajima D., Oh
Tanaka A., Kotani H., Nomura N., Ohara
"Prediction of the coding sequences of
The complete sequences of 100 new cDNA
code for large proteins in vitro.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                        015029
                                                              EMBL;
                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1456
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                                                                                                       SEQUENCE OF 1599-1906 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1506 MTPCILWIPNIHDV-DLEDRTTLAG
                Pfam;
                                                EMBL;
                                                                           Kim J.W., Lee Y., Hong Y.M., Hong M., Choe I.S.; Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                          DNA Res.
                                                                                                                                                                                                                                    MEDLINE=97349984; PubMed=9205841;
                                                                                                                                                                                                                                                     TISSUE=BRAIN;
                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606
                             InterPro; IPR000569; HECT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PLITLEMEARSSWPFFQHLDEIYGDQLEYVYDDTSLSVEVEE----EEDTSWGIEEWSLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SNWNLNLID-ISDLISLIPNPIDR-ITFSINTRHLSHTSKE----IYSFIRKRER---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---DTREDDEIEDQAEMDTRRDLDGIEYTHAIQDMI---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LDVLKHKLDELYPQGYPESVIQHLGYLFLKMSPEDIRK------WNVTSLETLKALLE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EKTACPSGKKAREIDESLIFYKKW----ELEACVDAALLATQMDRVNAIPF-----TYEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VCT-YLSRLSKDYGELQTELKKVKSLMIPSYTIELRKLMDRYPPSELNSFGLKNLFLVAM
                                             AB002310; BAA20771.1;
AF057569; AAC62492.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----VDKGHEMSPQAP---RRFL--PQVATLIDRFVKGRGQLDKD-----
                 PF00632;
                                                                                                                                          large proteins in vitro 4:141-150(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----IPNGYLVLDLSVQETLSG
PS50237; HECT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----VYGAWIDDKIESLLSTSVAIDDCDRGNLLQFSTLTLTTEKG
                HECT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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                                                                                                                                                                         unidentified human clones from brain v
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                                                                                                                                                                                                                    Seki N.,
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NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9P0A9;
Pfam;
SMART;
                 Ye M., Zhang Q.H., Zhou J., Shen Y., Wu X.Y., Fan H.Y., Mao Y.F., Dai M., Huang Q.H., Chen S "Human partial CDS from cd34+ stem cells."; Submitted (MAY-1999) to the EMBL/GenBank/DDBJ EMBL; AF161390; AAF28950.1; -
Pfam; PF00632; HECT; 1.
                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-JUN-2001 (TrEMBLrel. 17,
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                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                      TISSUE-BLOOD;
                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                       HSPC272 (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PARTLAGETGTESAPLGGVLTTPHNIS---SLSPRQLLGFPCAEVS--GLSTERVRELAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGGPPYGPPSTWSVSTMDALRGLLPVLGQPIIRSIPQGIVAAWRQRSSRDPSWRQPERTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QACTR---FFSRITKANVD------LLPRGAPERQRLLPAALACWGVRGSLLSEADV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----SSMHISSSLP-
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Pred. No. 2.2;
9; Mismatches 21:
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O1-MAY-2000 (TrEMBLrel. 1
AT2G28300 PROTEIN.
STRAIN=CV. COLUMBIA;
STRAIN=CV. COLUMBIA;
MEDLINE=20083487; PubMed=10617197;
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.
Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.Y
Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat |
Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Tallon L.J., Gill
Cronin L.A., Shen M., Vanaken S.E., Umayam L., Tallon L.J., Gill
                                                                                                                          Eukaryota; thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidaeurosids II; Brassicales; Brassicaceae; Arabidopsis NCBI_TaxID-3702;
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SEQUENCE
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Arabidopsis thaliana (Mouse-ear cress).
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; warmoliophyta; eudicotyledons; core eudicots; Rosid
                                                                              Q9AUB4 PRELIMINARY; PRT; 35
Q9AUB4;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last seque)
01-JUN-2001 (TrEMBLrel. 17, Last annot PUTATIVE CHROMATIN REMODELING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Copenhaver G.P., Preuss D., Nierman W.C., White O., Eis Salzberg S.L., Fraser C.M., Venter J.C.;
"Sequence and analysis of chromosome II of Arabidopsis Nature 402:761-768(1999).
EMBL; AC006202; AAD29825.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HPARTLA-----GETGTESAPLGGVLTTPHNISSLSPRQLLGFPCAEVSGLSTERVRE
                                                                                                                                                                                                                                          SKIETNSEELQASRTDEV---
                                                                                                                                                                                                                                                                   MDLAT----FMKLRTDAVLPLTVAEVQKLLGPHVEGLKAEERHRPVRD
                                                                                                                                                                                                                                                                                                                                 PQDLDTCDPRQLDVLYPKARLAFQN----MNGSEYFVKIQSFLGGAPTEDLKALSQQNVS
                                                                                                                                                                                                                                                                                                                                                               LTAKSSLEKCTADQLLGEKLSQEGETTPASDGETCHLAEETASSLSYVRSEPTASA----
                                                                                                                                                                                                                                                                                                                                                                                               VKGRGQLDKDTLDTL-----TAFYPGYLCSLSPEELSSV-----PPSSIWAVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                          HEMSPQAPRRPLPQVATL --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VGE--PSATTRTNVPD-----AQSPGEM----NLHTVETHKAEDSSGLKNQEALYNLSKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LDELYPQGYPESVIQHLGYLFLKMSPEDIRKWNVTSLETLK------ALLEVDKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SVAPDIHSSGSLSQEIRRDTSGTGGSARKQTADVTDVARVMKEI-----FSETSLLKHK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SRGETPKRQGKRRGQPLPATDASSARSTGLTPQIEVKVGNLSGTKAKFDAVAKEQPHFSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SSRDPSWRQPER----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALQGVTTAPSDATLPMSSQPSDATLPMSSQPVGSTVEAQEANVPSLPAALPAKRRVRNLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALRGL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----VQTLNVLENSSERKAFAVKKRPLTQGGGPVQNQNAVSSVCDGSKSPSEGRTYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EVLLPRLVSCPGPLDQDQQEAA-----RAALQGGGPPYGPPSTWSV-----STMD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RVPKAN-----EGSTSNPDQVSPVHSATTALRSDKAADKDL-----DAPPGFDSGSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RITKANVDLLPRGAPER-QRLLPAALACWGVRGSLLSEADVRALGGLACDLPGRFVAESA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VEGVLHGSNSSITQRTETATSLA------SDAEA-----TKFALPRSASEIVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HPTSSLALTSPDLSGPPGFQSLP------ASPAPTPIRGRGRGRGRSRGRGRR 217
                                                                                                                                                                                                                                                                                                                                                                                                                            DKLVSDIP-HPVPGDLTTSGSVANKDVDIGSSKVAAENELVKIPGGDVDSSVIQLSLGNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EVEKTACPSGKKAREIDESLIFYKKWELEACVDAALLATQMDRVNAIPFTYEQLDVLKHK
                                                                                                                                                                                                                                                                                                   STTAEPLPTDKL---EKNISFQDEVKTLNGD----KREAIL-----LSSEEQTNVN
                                                                                             (TrEMBLrel. 17, Created)
(TrEMBLrel. 17, Last sequence up
(TrEMBLrel. 17, Last annotation
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AA; 235758 MW;
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Pred. No. 5.7;
81; Mismatches
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                                                                                               on update)
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                       Rosidae;
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RESULT 15 Q9U5Y1

Q9U5Y1

PRELIMINARY;

PRT;

2015

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BARAR

Q9U5Y1; 01-MAY-2000 01-MAY-2000 01-JUN-2001

MICROTUBULE-ASSOCIATED PROTEIN CP224

(TrEMBLrel. 13, Created) (TrEMBLrel. 13, Last seq (TrEMBLrel. 17, Last ann

Last sequence up

update)

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Best Local Similarity
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"SPLAYED, a Putative Chromatin Remodeling Fact
"SPEDIATED, a Putative Chromatin Remodeling Fact
Reproductive Development in Arabidopsis.";

Submitted (MAR-2000) to the EMBL/GenBank/DDBJ
EMBL; AF247809; AAK31908.1; -.

SEQUENCE 3574 AA; 389826 MW; OCA25C1FF1AB6
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NCBI_TaxID=3702;
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                              514 LKALSQQNVSMDLAT----FMKLRTDAVLPLTVAEVQKLLGPHVEGLKAEERHRPVRD
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LSSEEQTNVNSKIETNSEELQASRTDEV-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RITKANVDLLPRGAPER-QRLLPAALACWGVRGSLLSEAD------VRALGGLA 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HPARTLA-----GETGTESAPLGGVLTTPHNISSLSPRQLLGFPCAEVSGLSTERVRE
                                                             EPTASA-
                                                                                                                           SVIQLSLGNTLTAKSSEEKCTADQLLGEKLSQEGETTPASDGETCHLAEETASSLSYVRS
                                                                                                                                                         ----IDRFVKGRGQLDKDTLDTL---
                                                                                                                                                                                        QEALYNLSKADKLVSDIP-HPVPGDLTTSGSVANKDVDIGSSKVAAENELVKIPGGDVDS 1987
                                                                                                                                                                                                                                                    FSETSLIKHKVGE--PSATTRTNVPD-----AQSPGEM---NLHTVETHKAEDSSGLKN 1928
                                                                                                                                                                                                                                                                               YEQLDVLKHKLDELYPQGYPESVIQHLGYLFLKMSPEDIRKWNVTSLETLK-----
                                                                                                                                                                                                                                                                                                                 VAKEQPHFSQSVAPDIHSSGSLSQEIRRDTSGTGGSARKQTADVTDVARVMKEI-----
                                                                                                                                                                                                                                                                                                                                                ----RPRFRREVEKTACPSGKKAREIDESLIFYKKWELEACVDAALLATQMDRVNAIPFT
                                                                                                                                                                                                                                                                                                                                                                                                            VAAWRQR---SSRDPSWRQPER-----TIL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                         KSPSEGRTYTALQGVTTAPSDATLPMSSQPSDATLPMSSQPVGSTVEAQEANVPSLPAAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----STMDALRGL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NSSERKAFAVKKRPLIQGVSSQHPGPNKQPLDLPVSTSSTLLGGGPVQNQNAVSSVCDGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HPTSSLALTSPDLSGPPGFQSLP------ASPAPTPIRGRGRGRSRGRGRGRR 1548
                                                                                          -PPSSIWAVRPQDLDTCDPRQLDVLYPKARLAFQN----MNGSEYFVKIQSFLGGAPTED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDLPGREVAESAEVLLPRLVS-CPGPLDQ--DQQEAARAALQGGGPPYGPPSTWSV----
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                                                             -STTAEPLPTDKL -- EKNISFQDEVKTLNGD--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3.6%;
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Pred.
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                                                                                                                                                         TAFYPGYLCSLSPEELSSV-----
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---PHVDGKSVDVANQTVKE
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2132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Graef R., Daunderer C., Schliwa M.;

Graef R., Daunderer C., Schliwa M.;

Dictyostelium DGCP224 is a microtubule-associated protein and a permanent centrosomal resident involved in centrosome duplication.";

Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AJ012088; CAB56504.1; -.

InterPro, IPR000357; HEAT_repeat.

PROSITE: PS50077; HEAT_REPEAT; 1.

SEQUENCE 2015 AA; 224038 MW; BA64E982ADDC92EE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
NCBI_TaxID-44689;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-AX2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
216 DQ-----FEKLPTDPAVPLKYTRSEAAKALANASKGIQAK 250
                                 519 QQNVSMDLATFMKLRTDAVLPL--TVAEVQKLLGPHVEGLKAE 559
                                                                                                          477 RQLDVLYPKARLA--FQNMN------GSEYFVKIQSFLGGA-------PTEDLKALS 518
                                                                                                                                                                                                                                                                                                                             157 KQIPVKLILKQFSPWFENRDKGIRDQASELFIEIYRWIGKALIPLISEALTPIQ-LKALQ 215
                                                                                                                                                                                           448
                                                                                                                                                                                                                                                  394 -KALLEVDKGHEMSPQAPRRPLPQVATLIDRFVKGRGQLDKDTLTAFYPGYL-----
                                                                                                                                                    98 ASTRPRAKEKTIECLLLTIEADSAEPVVEALLKGTSSTSPKILLASL-AALTQALKTFGP 156
                                                                                                                                                                                                                             52 FKKILA-----DINPMSQERALEPLSAFIDRC------DCVNKFAASYVGVLVEKLF 97
                                                                                                                                                                                                                                                                                                          w
                                                                                                                                                                                         ------SSIWAVRPQDLDTCDP 476
                                                                                                                                                                                                                                                                                                    DEEAPSGSIEDRINHKNW-----KWRVSGLEELTTKFRNSIEGSGPLFNEWGPQ 51
                                                                                                                                                                                                                                                                                                                                                                                                                  DB 5;
                                                                                                                                                                                                                                                                                                                                                                               74;
                                                                                                                                                                                                                                                                                                                                                                                                                  Length 2015;
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                                                                                                                                                                                                                                                                  447
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Search completed: December 7, 2001, 09:53:43
Job time: 326 sec

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